

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd..

OM protein - protein search, using sw model

Run on: August 24, 2001, 17:32:30 ; Search time 32.57 Seconds
(without alignments)
787.349 Million cell updates/sec

Title: US-09-532-263-5

Perfect score: 2282

Sequence: 1 MSSCSGLSLVAVATLV.....KPGFLASVIPVDRRPGAPNL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

al number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

```

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2282	100.0	423	17 AAR92814	Human interleukin-
2	2257.5	98.9	422	17 AAR90900	Human interleukin-
3	2257.5	98.9	422	22 AAB36654	Human IL-11 recept
4	1879.5	82.4	432	17 AAR92813	Murine interleukin
5	1853.5	81.2	432	22 AAB36653	Mouse IL-11 recept
6	1813.5	79.5	441	17 AAR99091	Murine Etl-2 gene
7	1662.5	72.9	379	21 AAY59390	Murine soluble int
8	402	17.6	460	13 AAR2616	IL-6R for soluble
9	402	17.6	460	22 AAB36656	Mouse IL-6 recept
10	389	17.0	460	12 AAR13318	IL-6 receptor, Mu
11	370.5	16.2	468	17 AAR98364	Interleukin-6 rece

12	367.5	16.1	468	10 AAP90284	Sequence of a rece
13	367.5	16.1	468	14 AAR37215	IL-6 receptor. Sy
14	367.5	16.1	468	22 AAB36655	Human IL-6 recepto
15	366.5	16.1	372	13 AAR20024	Ciliary neurotroph
16	366.5	16.1	372	14 AAR37820	Sequence of human
17	366.5	16.1	372	16 AAR70147	Human recombinant
18	358.5	15.7	468	10 AAR90525	B cell stimulating
19	357.5	15.7	468	19 AAP71371	Human interleukin-
20	346.5	15.2	1158	21 AAY92205	Fusion polypeptide
21	343	15.0	525	18 AAW36846	Human fusion polyp
22	339.5	14.9	1168	21 AAY92204	Fusion polypeptide
23	338	14.8	543	20 AAY03164	Chimeric sIL-6R/IL
24	337.5	14.8	344	10 AAR90528	B cell stimulating
25	337.5	14.8	345	21 AAY55071	SR345 protein sequ
26	337	14.8	360	20 AAW70804	Amino acid sequenc
27	337	14.8	360	21 AAY92199	Soluble human IL-6
28	337	14.8	468	21 AAY92196	Human IL-6R-alpha-
29	337	14.8	477	21 AAY92197	Human IL-6R-alpha-
30	337	14.8	592	20 AAW70797	Human interleukin-
31	337	14.8	592	21 AAY92185	Human IL-6R-alpha-
32	337	14.8	690	21 AAY92195	Human IL-6R-alpha-
33	330	14.5	515	21 AAB15404	IL-6R/IL-6 fusion
34	328.5	14.4	323	10 AAP90527	B cell stimulating
35	324	14.2	1042	16 AAR70122	IL8-R type 1-GBP 1
36	323.5	14.2	325	21 AAB15389	Human interleukin
37	323.5	14.2	325	21 AAB15390	Bovine interleukin
38	322.5	14.1	315	20 AAW70805	Amino acid sequenc
39	322.5	14.1	315	21 AAY92200	Soluble human IL-6
40	307.5	13.5	326	15 AAR58304	Rat ciliary neutro
41	307.5	13.5	500	18 AAW36847	Human fusion polyp
42	261.5	11.5	228	22 AAB36651	Mouse cytokine rec
43	247	10.8	229	18 AAW09779	Epstein barr virus
44	244	10.7	229	19 AAW53624	Epstein barr virus
45	244	10.7	229	22 AAB36652	Human cytokine rec

ALIGNMENTS

RESULT 1

AAR92814
ID AAR92814 standard; Protein; 423 AA.

XX AC AAR92814;

XX DT 21-MAY-1996 (first entry)

XX DE Human interleukin-11 receptor alpha chain.

XX KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..23

FT Protein /label= Sig_peptide

FT Domain /label= Mat_protein

FT Domain /label= 24..366

FT FT /label= Extracellular_domain
FT FT /note= "the extracellular domain includes
FT FT haemopoietin and Ig-like domains"

FT Domain 367..392

FT FT /label= Transmembrane_domain

FT Domain 393..423

XX FT /label= Cytoplasmic_tail

PN WO9607737-A1.

XX PD 14-MAR-1996.

XX PD 05-SEP-1995;

PF 95WO-AU00578.

```

XX 05-SEP-1994; 94AU-0007902.
PR 05-SEP-1994; 94AU-0007901.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Hilton DJ;
XX
XX WPI: 1996-171612/17.
XX N-PSDB; AAT17869.
XX
XX Nucleic acid encoding haemopoietin receptor containing conserved
XX amino acid motif esp. IL-11 receptor alpha chain - used for
XX developing IL-11 (ant)agonists
XX
XX Claim 8; Page 47-49; 87pp; English.
XX
XX The human interleukin-11 (IL-11) receptor alpha chain (AAR92814)
XX was identified by expression of DNA (AAT17869) isolated from human
XX bone marrow cDNA libraries. Expression of the human IL-11
XX receptor alpha chain results in specific binding of human IL-11
XX and permits IL-11 signalling. The receptor alpha chain can be used
XX to develop agonists or antagonists of therapeutic appin. or in
XX the treatment or diagnosis of conditions involving a deficiency of
XX IL-11, excess IL-11 or aberrant effects of normal endogenous IL-11
XX levels.
XX
XX Sequence 423 AA;
XX
XX Query Match 100.0%; Score 2282; DB 17; Length 423;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-150;
XX Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MSSSCGSLSRVLVAVATALVSASSPCPAWGPVQYQPGRSVKLCCPGVTAGDPVSWF 60
Db 1 mssscgslsrvlavatalvsasspcpawgpgvqyqpggrsvklccpgvtagdpsvswf 60
Qy 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVWSC 120
Db 61 rdgepkllqgpdsglghehlvlaqadstdegtyicqlodgalggtvtlqlypparpvpsc 120
Qy 121 QAADYENFSCWSPSQISGLPTRYLTSYRKTKVLGADSQRRSPSTGPMPCQDPLGAARC 180
Db 121 qaadyenfscwspsqisglptryltsyrkktvlgadsqrrspstgpmwpcqdpplgaarc 180
Qy 181 VVHGAEFWSQYRINVTENPVGCGASTRLLDVSLQSLRPDPQGLRVESVPGYRGLRAS 240
Db 181 vvhdgefswqyrinvtvnpvggastrlldvslqslrpdppqglrvsvpgyprglras 240
Qy 241 WTPASWPCQPHFLKRLQYRPAQHPAWSVVEPAGLEEVITDVAGLPHAVRVSARDFL 300
Db 241 wtpaswpcqphflkrlqyrpqhpawstvepagleevitdavglpahavrvsardfl 300
Qy 301 DAGWSTWSBPAWGTPSTGTIPKEIPAWGQLHTQPEVEPQVDSPPAPRPSLQPHRLDH 360
Db 301 dagtwstwsbpaugtptgtipkeipawqlhtqpevepqvdsppaprpsslqphrlldh 360
Qy 361 RDSVEQAVLASLGLSLFLGVLVAGALGLWLRLRGKQSGPKPGFLASVIPPVDRRPGA 420
Db 361 rdsveqvavlaslglsflglvagalglwlrlrrgkdgspkpgflasvipvdrprga 420
Qy 421 PNL 423
Db 421 pnl 423
XX
XX RESULT 2
XX AAR99090
XX ID AAR99090 standard; Protein: 422 AA.
XX
XX AC AAR99090;
XX

```

```

DT 09-OCT-1996 (first entry)
XX Human interleukin-11 receptor.
DE
XX
KW Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;
KW osteoporosis; Paget disease; myeloma.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX Protein 24..422
XX Domain 24..365
XX Region 24..111
XX Region 112..365
XX Region 366..390
XX Domain 391..422
XX Domain 391..422
XX W09619574-A1.
XX
XX 27-JUN-1996.
XX
XX 27-NOV-1995; 95WO-US15400.
XX
XX 22-DEC-1994; 94US-0362304.
XX
XX (GEMY ) GENETICS INST INC.
XX
XX Tobin JF;
XX
XX WPI: 1996-309588/31.
XX N-PSDB; AAT33278.
XX
XX New nucleic acid encoding human interleukin 11 receptor - and
XX related protein, antibodies, receptor antagonists, etc, useful for
XX treating and preventing loss of bone mass
XX
XX Claim 13; Page 35-37; 54pp; English.
XX
XX Human interleukin-11 (IL-11) receptor (AAR99090) is thought to play a
XX role in the regulation of bone maturation and repair. Its amino
XX acid sequence was deduced from a cDNA clone (AAT33278) isolated from
XX a human activated peripheral blood mononuclear cell cDNA library.
XX Recombinant IL-11 receptor or its fragments, pref. amino acids
XX 24-422, 24-365 (soluble extracellular domain), 391-422, 102-422 or
XX 102-365, can be expressed in host cell systems. It is used to
XX treat/prevent loss of bone mass (e.g. osteoporosis, Paget's disease,
XX multiple myeloma or hypogonadal conditions), as well as immune
XX diseases and cancer.
XX
XX Sequence 422 AA;
XX
XX Query Match 98.9%; Score 2257.5; DB 17; Length 422;
XX Best Local Similarity 99.5%; Pred. No. 1.4e-148;
XX Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MSSSCGSLSRVLVAVATALVSASSPCPAWGPVQYQPGRSVKLCCPGVTAGDPVSWF 60
Db 1 mssscgslsrvlavatalvsasspcpawgpgvqyqpggrsvklccpgvtagdpsvswf 60
Qy 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVWSC 120
Db 61 rdgepkllqgpdsglghehlvlaqadstdegtyicqlodgalggtvtlqlypparpvpsc 120
Qy 121 QAADYENFSCWSPSQISGLPTRYLTSYRKTKVLGADSQRRSPSTGPMPCQDPLGAARC 180

```

```
Db 121 qaadyenfsctwpsqisglptryitsyrkktvlgadsqrrspstgppwpcpdpigaarc 180
Qy 181 VVHGAEFWQSYRINTEVNPLGASTRLLDVSLQSLRDPDQGLRVESVPGYPRGLRAS 240
Db 181 vvhgafesqyrinvtevnpl-gastrlldvslqslrpdpggrrvesvpyprlras 239
Qy 241 WTPASWPCQPHFLKFRLOQYRPAQHAPAMSTVEPAGLEEVITDAVAGLPHAVRVVSARDFL 300
Db 240 wtpaswpcqphflkfrlqyrpaqhpawstvepagsleevitdavaglpavrvvsardfl 299
Qy 301 DAGTWTWSPAEWGTPTGTIPKEIPAMGOLHTQPEVEPQVDSAPPRLSLOPHRLLDH 360
Db 300 dagtwtwspeawgtptgtipkeipawgqlhtqvevpqvdspapprrslqphprlldh 359
Qy 361 RDSVEQVAVLASIGLSIFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGA 420
Db 360 rdsveqvavlasiglsiflgvlagalalglwlrirrgkdgspkpgflasvipvdrpaga 419
421 PNL 423
420 pnl 422

RESULT 3
AAB36654
ID AAB36654 standard; Protein; 422 AA.
XX
AC AAB36654;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human IL-11 receptor subunit alpha protein SEQ ID NO:11.
XX
KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW modulating cell proliferation; diagnosis; detection; drug screening;
XX immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200073451-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US14867.
XX
PR 01-JUN-1999; 99US-0322913.
(SCHE ) SCHERING CORP.
Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
WPI: 2001-061536/07.
XX
XX Novel composition comprising DNAX cytokine receptor subunit polypeptide
XX useful for regulating immune system function and for treating
XX immunological disorders
XX
XX Disclosure; Page 13-15; 93pp; English.
XX
XX The present invention describes a composition (I) comprising a
XX recombinant DNAX cytokine receptor subunit-2 (DCRS2), polypeptide.
XX The DCRS2 polypeptide is useful for binding ligands and for preparing
XX antibodies. The DCRS2 polypeptide is also useful for modulating cell
XX proliferation, for diagnostic and therapeutic applications, for
XX detecting presence of their ligands and in drug screening assays. It
XX is also useful for treating conditions such as immunological disorders.
XX The present sequence represents a cytokine receptor subunit protein
XX which is given in an alignment of various cytokine receptor subunits in
XX the exemplification of the present invention.
XX
SQ Sequence 422 AA;
```

```
Query Match 98.9%; Score 2257.5; DB 22; Length 422;
Best Local Similarity 99.5%; Pred. No. 1.4e-148;
Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MSSSCGSLRVLAVATALVSASSPCQAWGPPGVQYQOPGRSVKLCPCGVTAGDPVSWF 60
Db 1 mssscgslrvlavatalvsasspcqawgppgvqyqgrsvklccpgvtagdpvswf 60
Qy 61 RDGEPKLLQGGPDGSLGHELVLAQADSTDEGTICOTLDGALGTTVTLQGLGYPPARPVWSC 120
Db 61 rdgepkllqgpdsglghelvlaqadstdegticytldgalgvtvltlqgypparvpsc 120
Qy 121 QAADYENFSCWSPSOISGLPTRYITSYRKKTVLGADSORRSPSTGWPWCPQDPGLGAARC 180
Db 121 qaadyenfscwspqisglptryitsyrkktvlgadsqrrspstgppwpcpdpigaarc 180
Qy 181 VVHGAEFWQSYRINTEVNPLGASTRLLDVSLQSLRDPDQGLRVESVPGYPRGLRAS 240
Db 181 vvhgafesqyrinvtevnpl-gastrlldvslqslrpdpggrrvesvpyprlras 239
Qy 241 WTPASWPCQPHFLKFRLOQYRPAQHAPAMSTVEPAGLEEVITDAVAGLPHAVRVVSARDFL 300
Db 240 wtpaswpcqphflkfrlqyrpaqhpawstvepagsleevitdavaglpavrvvsardfl 299
Qy 301 DAGTWTWSPAEWGTPTGTIPKEIPAMGOLHTQPEVEPQVDSAPPRLSLOPHRLLDH 360
Db 300 dagtwtwspeawgtptgtipkeipawgqlhtqvevpqvdspapprrslqphprlldh 359
Qy 361 RDSVEQVAVLASIGLSIFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGA 420
Db 360 rdsveqvavlasiglsiflgvlagalalglwlrirrgkdgspkpgflasvipvdrpaga 419
Qy 421 PNL 423
Db 420 pnl 422

RESULT 4
AAR92813
ID AAR92813 standard; Protein; 432 AA.
XX
AC AAR92813;
XX
DT 21-MAY-1996 (first entry)
XX
DE Murine interleukin-11 receptor alpha chain.
XX
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW therapy; diagnosis.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..23 /label= Sig_peptide
FT Protein 24..432 /label= Mat_protein
FT Domain 24..367 /label= Extracellular_domain
FT /note= "the extracellular domain includes haemopoietin and Ig-like domains"
FT Domain 368..393 /label= Transmembrane_domain
FT Domain 394..432 /label= Cytoplasmic_tail
WO9607737-A1.
14-MAR-1996.
05-SEP-1995; 95WO-AU00578.
XX
XX
```

PR 05-SEP-1994; 94AU-0007902.
 PR 05-SEP-1994; 94AU-0007901.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Hilton DJ;
 XX WPI; 1996-171612/17.
 DR N-PSDB; AAT17868.
 XX Nucleic acid encoding haemoipoietin receptor containing conserved
 PT amino acid motif esp. IL-11 receptor alpha chain - used for
 PT developing IL-11 (ant)agonists
 XX
 PS Claim 6; Page 42-44; 87pp; English.
 XX
 CC The murine interleukin-11 (IL-11) receptor alpha chain Nrl
 CC (AAR92813) was identified by expression of DNA (AAT17868) isolated
 CC from adult mouse liver cDNA libraries. Nrl is a low affinity
 CC receptor for IL-11 and interacts with gp130 to generate a high
 CC affinity IL-11 receptor. IL-11 can be used to develop
 CC agonists or antagonists of therapeutic appln. or in the treatment
 CC or diagnosis of conditions involving a deficiency of IL-11,
 CC excess IL-11 or aberrant effects of normal endogenous IL-11
 CC levels.
 XX
 SQ Sequence 432 AA;

Query Match 82.4%; Score 1879.5; DB 17; Length 432;
 Best Local Similarity 83.1%; Pred. No. 2e-122;
 Matches 353; Conservative 18; Mismatches 51; Indels 3; Gaps 2;

Qy 1 MSSCSGLSRVLVAVATALVSASSPCPAWGPVQVQGRSVKLCPCGVTAGDPVSWF 60
 Db 1 msscsgrltrvlavatalvssspcpqawpgvqyqgprpvmclccpgvsagtpswf 60
 Qy 61 RDGPKLLQGPDGSLGHELVLAQADSTDEGTYICQTLGALGGTTLQLGYPARPVSC 120
 Db 61 rdgdrllqgpdsglghrlvlaqvdsdpgtyvcqtdlgvsggmvtiklgfpparpevc 120
 Qy 121 QAADYENFSCWSPQSISGLPTRYLTSTYRKTKVLGADSORSPSTGPMPCDPLGAARC 180
 Db 121 qavdyenfscwspqvgvsglptryltsyrkktlpgaesqrespgwpcqdplesarc 180
 Qy 181 VVHGAEFWSQYRINVTENPLGGASTRLLDVSLQSLRPDPQGLRVESVPGYRGLRAS 240
 Db 181 vvghaefwseyrinvtenvnpl-gastclldvrlsrlrppqglrvsvpgyprrlhas 239
 Qy 241 WTPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVSARDFL 300
 Db 240 wtpaswrrqphflkfrlqyrpachpawstvepgleevitdavaglphavrsardfl 299
 Qy 301 DAGTWSWSPAWGTPSTGTIPKEIPAWQLHTQ--PEVEPQVDSPPAPRPSLOPHRLL 358
 Db 300 dagtwsawspeawgtpstgtpideipdwsqghgqgleavagedsaparpqlpdrpl 359
 Qy 359 DHRDSVEQAVLASIGLISFLGVLVAGALGLWLRLRGKDGSPKPGFLASVIPVDRRP 418
 Db 360 dhrdpqevavlasiglfisciglavgalglwlrlrrsgkdgqpkqgllapmpivekpl 419
 Qy 419 GAPNL 423
 Db 420 gipnl 424

RESULT 5

AAB36653
 ID AAB36653 standard; Protein; 432 AA.
 XX
 AC AAB36653;
 XX
 DT 13-MAR-2001 (first entry)

XX Mouse IL-11 receptor subunit alpha protein SEQ ID NO:10.
 DE
 XX
 KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
 KW modulating cell proliferation; diagnosis; detection; drug screening;
 KW immunological disorder.
 XX
 OS Mus sp.
 XX
 PN WO200073451-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAY-2000; 2000WO-US14867.
 XX
 PR 01-JUN-1999; 99US-0322913.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan EJ;
 XX
 DR WPI; 2001-061536/07.
 XX
 CC Novel composition comprising DNAX cytokine receptor subunit polypeptide
 CC useful for regulating immune system function and for treating
 CC immunological disorders
 XX
 PS Disclosure; Page 13-15; 93pp; English.
 XX
 CC The present invention describes a composition (I) comprising a
 CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
 CC The DCRS2 polypeptide is useful for binding ligands and for preparing
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
 CC proliferation, for diagnostic and therapeutic applications, for
 CC detecting presence of their ligands and in drug screening assays. It
 CC is also useful for treating conditions such as immunological disorders.
 CC The present sequence represents a cytokine receptor subunit protein
 CC which is given in an alignment of various cytokine receptor subunits in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 432 AA;

Query Match 81.2%; Score 1853.5; DB 22; Length 432;
 Best Local Similarity 82.1%; Pred. No. 1.2e-120;
 Matches 349; Conservative 19; Mismatches 54; Indels 3; Gaps 2;

Qy 1 MSSCSGLSRVLVAVATALVSASSPCPAWGPVQVQGRSVKLCPCGVTAGDPVSWF 60
 Db 1 msscsgrltrvlavatalvssspcpqawpgvqyqgprpvmclccpgvsagtpswf 60
 Qy 61 RDGPKLLQGPDGSLGHELVLAQADSTDEGTYICQTLGALGGTTLQLGYPARPVSC 120
 Db 61 rdgdrllqgpdsglghrlvlaqvdsdpgtyvcqtdlgvsggmvtiklgfpparpevc 120
 Qy 121 QAADYENFSCWSPQSISGLPTRYLTSTYRKTKVLGADSORSPSTGPMPCDPLGAARC 180
 Db 121 qavdyenfscwspqvgvsglptryltsyrkktlpgaesqrespgwpcqdplesarc 180
 Qy 181 VVHGAEFWSQYRINVTENPLGGASTRLLDVSLQSLRPDPQGLRVESVPGYRGLRAS 240
 Db 181 vvghaefwseyrinvtenvnpl-gastclldvrlsrlrppqglrvsvpgyprrlhas 239
 Qy 241 WTPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVSARDFL 300
 Db 240 wtpaswrrqphflkfrlqyrpachpawstvepgleevitdavaglphavrsardfl 299
 Qy 301 DAGTWSWSPAWGTPSTGTIPKEIPAWQLHTQ--PEVEPQVDSPPAPRPSLOPHRLL 358
 Db 300 dagtwsawspeawgtpstgtpideipdwsqghgqgleavagedsaparpqlpdrpl 359
 Qy 359 DHRDSVEQAVLASIGLISFLGVLVAGALGLWLRLRGKDGSPKPGFLASVIPVDRRP 418
 Db 359 dhrdpqevavlasiglfisciglavgalglwlrlrrsgkdgqpkqgllapmpivekpl 419

Db 360 dhrdpleqvavlaslgifsciglavgalalglwlrlrrskgqpkpqlapmipveklp 419
 QY 419 GAPNL 423
 Db 420 gipnl 424

RESULT 6
 AAR99091 standard; Protein; 441 AA.
 AC AAR99091;
 XX
 XX 09-OCT-1996 (first entry)
 DT
 XX Murine Etl-2 gene product.
 DE
 XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;
 KW osteoporosis; Paget disease; myeloma; Etl-2.
 KW

Mus sp.
 PN WO9619574-A1.
 XX
 XX 27-JUN-1996.
 PD
 XX
 XX 27-NOV-1995; 95WO-US15400.
 PF
 XX 22-DEC-1994; 94US-0362304.
 PR
 XX (GEMY) GENETICS INST INC.
 PA
 XX Tobin JF;
 PI
 XX WPI: 1996-309588/31.
 DR N-PSDB; AAT32613.
 DR
 XX New nucleic acid encoding human interleukin 11 receptor - and
 PT related protein, antibodies, receptor antagonists, etc, useful for
 PT treating and preventing loss of bone mass
 PT
 XX Example 1; Page 37-40; 54pp; English.
 PS
 XX The amino acid sequence of the murine Etl-2 gene product is given
 CC in AAR99091. Probes based on the Etl-2 gene (AAT32613) were used
 CC to screen a human cDNA library, yielding a cDNA clone (AAT33278) that
 CC coded for human interleukin-11 receptor (AAR99090), a protein
 CC involved in bone maturation and repair.

Sequence 441 AA:
 Query Match 79.5%; Score 1813.5; DB 17; Length 441;
 Best Local Similarity 82.7%; Pred. No. 7.4e-118;
 Matches 339; Conservative 17; Mismatches 51; Indels 3; Gaps 2;

QY 16 ATALVSASSPCQAWGPPGVQYQPGRSVKLCPCGVTAGDPVSWFRDGEKLLQGDPSGL 75
 Db 25 atalvsasspcqawppgvqyqgprpvmccpgvsgatpvsftrdgsrllqgpdsgl 84
 QY 76 GHELVLQAQDSTDEGNYICQTLGALGGVTTLQLGTPPARPVVSCQADYENFSCWSPS 135
 Db 85 ghrlvlaqvdsdgytyvcqltdgvggmvtlklgfpaprpevcqadvfensctwspg 144
 QY 136 QISGLPTRYLTYSRKKTVLGADSORSPSGPWPQDPLGAARCVVHGAEFWSOYRINV 195
 Db 145 qvsglptryltsyrkkclpqaesqrespsgypwpcqdpqleasrcvvhgafwseyrinv 204
 QY 196 TEVNPGLGASTRLDVSQILRPDPQGLRVESVPGYPRGLRASWTYPASWPCQPHFL 255
 Db 205 tevnpl-gastclldvrlsqilrpdppqglrvsvpgyprllhaswtypaswrqphfl 263
 QY 256 KFRLOVRPAQHPAMSTVERAGLEEVITDAVAGLPHAVRVSARDFLDAGTWTWSPEAWGT 315

Db 264 kfrlqyrpqahpawstvepigliveeltdavaglpahavrvsarofldagtwsapeawgt 323
 QY 316 PSTGTIPKEIPAMQQLHTQ--PEVEPQVDSPPAPRPSLOPHPRLLDHRDSVEQVAVLASL 373
 Db 324 pstgplqdeipdwsgqhgqleavvaqedsaparpqlgdpdrldhrdpleqvavlasl 383
 QY 374 GILSFTGLVAGALALGLWLRLRRGGDKSPKPGFLASVIPVDRRPGAPNL 423
 Db 384 gifsciglavgalalglwlrlrrsgkdqpkpqlapmipveklpgipnl 433

RESULT 7
 AAY59390 standard; Protein; 379 AA.
 AC AAY59390;
 XX
 XX 14-MAR-2000 (first entry)
 DT
 XX Murine soluble interleukin-11 receptor.
 DE
 XX Interleukin-11; IL-11; IL-11R; human; bone density disorder; gp130;
 KW IL-11 tertiary complex; glycoprotein 130; postmenopausal bone loss;
 KW bone resorption inhibitor; bone formation; therapy.
 XX
 XX Mus sp.
 XX WO9959608-A2.
 PN
 XX 25-NOV-1999.
 PD
 XX 19-MAY-1999; 99WO-CA00516.
 PF
 XX 19-MAY-1998; 98CA-2237915.
 PR
 XX (HAMI-) HAMILTON CIVIC HOSPITAL RES DEV CORP.
 PA
 XX Shaughnessy S, Austin RC;
 PI
 XX WPI: 2000-062377/05.
 DR N-PSDB; AA240400.
 DR
 XX Inhibiting formation of a tertiary complex for the treatment of
 PT osteoporosis
 PT
 XX Example 3; Page 46-50; 61pp; English.
 PS
 XX This sequence is the soluble mouse interleukin-11 receptor (IL-11R).
 CC The invention relates to a method of treating or alleviating the symptoms
 CC of a pathological condition in which bone density is decreased comprises
 CC inhibiting the formation of a tertiary complex of IL-11, IL-11 receptor
 CC and glycoprotein 130 (gp130) in a mammalian patient suffering from such a
 CC condition. The method is used to treat or alleviate the symptoms of a
 CC pathological condition in which bone density is decreased, especially
 CC postmenopausal bone loss. The IL-11 binding peptide is useful in the
 CC purification of IL-11 or in depleting IL-11 from a solution. TRAP
 CC (tartrate-resistant acid phosphatase) and bone marrow formation assays
 CC can be used for the identification of IL-11 antagonists. The method not
 CC only inhibits bone resorption and hence bone loss, but also increases the
 CC process of bone formation to increase bone density.
 XX
 SQ Sequence 379 AA;

Query Match 72.9%; Score 1662.5; DB 21; Length 379;
 Best Local Similarity 83.7%; Pred. No. 1.7e-107;
 Matches 309; Conservative 17; Mismatches 40; Indels 3; Gaps 2;

QY 1 MSSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQPGRSVKLCPCGVTAGDPVSWF 60
 Db 1 mssscsgltrvlvavatalvsssspcqawgppgvqyqgprpvmccpgvsgatpvsf 60

QY 61 RDGEPLKQGDGSLGHELVLAQADSTDEGTICOTLDGALGTTVLQGYPPARPVWSC 120
Db 61 rdgdrllqgpdsglghklvlaqvdsdpdegtyvcqtdlgvsggmvtlklgfpaprevsc 120
QY 121 QAADYENSCWSPSQISGLPTRYLTSYRKTKTVLGADSORRSPSTGPPCPDPLGAARC 180
Db 121 qadvyenfscwspdgqsglptryltsyrkktlpgaesqrespstgppcpdpplgaarc 180
QY 181 VVHGAEFWSQYRINTEVNPGLGASTRLLDVLSQILRPDPQGLRVESVPCYPRGLRAS 240
Db 181 vvhgafwseayrinvevnppl-gastclldvrlqslrpdpgqglrvsvpsyprrlhas 239
QY 241 WTYPASWPCQPHFLKFRQYPAQHPAMSTVEPAGLEEVITDAVAGLPHAVRVSGARDFL 300
Db 240 wtypaswrqphflkfrlqyraqhpawstvepgleevitdavagiphavrvsardfl 299
QY 301 DAGTWSWSPAWGTPTGTIPKEIPANGQLHTQ--PEVEPOVDSPPAPRPSLQPHRLL 358
Db 300 dagtwsawspeawgtptgstplqdeipdwsqghgqgleavvaqedsaparpalsqdprrpl 359
359 DHRDSVEQV 367
Db 360 dhrdpleql 368

RESULT 8
AAR22616
ID AAR22616 standard; Protein; 460 AA.
AC AAR22616;

DT 04-NOV-1992 (first entry)
DE IL-6R for soluble IL-6R prodn.
XX Soluble; sIL-6R.

KW Mus musculus.
OS
XX

Key Location/Qualifiers
FT Peptide 1..19
FT Region /label= sig_peptide
FT 358..385
FT /note= "see CC"

PN JP04099800-A.
XX 31-MAR-1992.

17-AUG-1990; 90JP-0215886.

17-AUG-1990; 90JP-0215886.

(CHUS) CHUGAI PHARM CO LTD.
PA (TOYJ) TOSOH CORP.

WPI; 1992-157367/19.
DR P-FSDB; AAR22616.

Recombinant mouse IL-6 receptor - prepd. by culturing host
transformed by expression vector contg. DNA coding the protein,
and collecting soluble prod.

PS Disclosure; Fig 7(1-2); 9pp; Japanese.

XX The sequence is the full-length mouse IL-6 receptor.
CC The region comprising amino acids 358-385 (see feature table)
CC is indicated but not labelled in the sequence given in the
CC specification. The sequence is used in the prodn. of a sol.
CC mouse IL-6 receptor protein (sIL-6R) which binds specifically to
IL-6 and has no intracellular region.

XX Sequence 460 AA;

Query Match 17.6%; Score 402; DB 13; Length 460;
Best Local Similarity 30.6%; Pred. No. 3.5e-20;
Matches 144; Conservative 55; Mismatches 184; Indels 88; Gaps 23;

QY 1 MSSSCSGLSRVLAVATATVLSASSPCPOAWGPPGVQYQGPGRSVKLCPCGVTAGDPVS-- 58
Db 2 ltvgctllvallaapavalvigs--cralevangtvtslpgatvtllcpgkaagnvth 59
QY 59 WFRDGEPLKQGDGSLGHELVLAQADSTDEGTICOTLDGALGTTVLQGYPPARPV 117
Db 60 wtygs--gnrewtttgnltvldvqlsdtgdlc-slndhltvgtvpllvdppeepk 114
QY 118 VSC-QAADYENFSCWSPSQISGLPTRYLTSYRKTKTVLGADSORRSPSTGPPCP- 175
Db 115 iscfknplvnaicewrpsstps-pttkavifakk1-----ntngksdfqvpccysqql 168
QY 176 GAARCVVHGAEFWSQYRI-NVTEVNPGLGASTRLLDVLSQILRPDPQGLRVESVPGYP 234
Db 169 kafscqveilegdkvyhivslcvansvgkseshneafhslkmvqpdpnanlvvsai 228
QY 235 RGLRASWTPASWPCQPHFLKFRQYPAQHPAMS-----TVEPAGLEEVITDAVAGL 288
Db 229 rwlkvswdhpwtw-psyvllqfqlryr---pwwskftvlllpvagvqcvihdalrgv 283
QY 289 PHAVRVSGARDFLDAGTWSWSPAWGTPTGTIPKEIPA--WGQLHTQPEVEPOVDS 345
Db 284 khvvgvrgkeeldlgqswsewspvgtptwlae-prttpagllwnp--tqvsve---ds-- 335
QY 346 PPRPSLQPHRLLDHRD----SVEQVAVLA-----SLGILSFLGLVAGALGLW---- 391
Db 336 -----anhedqyesateatsvlapvqessmslptfl-vagsglafglllcvf 382
QY 392 --LRLRRGKD-----GSPKPGFLASVVPVDRRRPGAPN 422
Db 383 ilrlrlkqwkseakeksttppppyslgplkptflvllphtphssgsdn 433

RESULT 9

AAB36656
ID AAB36656 standard; Protein; 460 AA.

AC AAB36656;

DT 13-MAR-2001 (first entry)

Mouse IL-6 receptor subunit alpha protein SEQ ID NO:13.

DNAX cytokine receptor subunit; DCRS2; receptor protein;
modulating cell proliferation; diagnosis; detection; drug screening;
immunological disorder.

Mus sp.

WO200073451-A1.

07-DEC-2000.

30-MAY-2000; 2000WO-US14867.

01-JUN-1999; 99US-0322913.

(SCHE) SCHERING CORP.

Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;

WPI; 2001-061536/07.

Novel composition comprising DNAX cytokine receptor subunit polypeptide
useful for regulating immune system function and for treating
immunological disorders

Db 222 itvtavarnprwlsvtwqphsw-n-ssfyrlrfelyraersktfttmvkdqlqhcvh 280
 QY 283 DAVAGLPHAVRSARDFLDAGTWTSTWSPAWGTPSTGTIPKEIPAWGQLHTQPEVEPQVD 342
 Db 281 dawsglrhvvtqlraeqefggewsewseamgtptwtes-----rspaenevs 328
 QY 343 SPAPPRPSLOPHRLDHRDSVEQVAV-----LASLGILSFLGLVAGALALG----- 389
 Db 329 tpmqalttkddnll-frdsanatslpvqdsstsvlptfl-vagsglafgtllciaivl 386
 QY 390 ----LW-LRLRRGGKDGSPKPGFLASVIPVDRRP 418
 Db 387 rfkktwklralkegktsmhpypslgqlvperprp 420

RESULT 13
 AAR37215
 ID AAR37215 standard; Protein; 468 AA.
 XX
 AC AAR37215;
 XX
 DE IL-6 receptor.
 XX
 KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
 KW transmembrane; multiple myeloma; binding; ability; signal transfer;
 KW disease; intracellular.
 XX
 OS Synthetic.
 XX
 PN JP05091892-A.
 XX
 PD 16-APR-1993.
 XX
 PF 02-OCT-1991; 9LJP-0255521.
 XX
 PR 02-OCT-1991; 9LJP-0255521.
 XX
 PA (CHUS) CHUGAI PHARM CO LTD.
 PA (KISH/) KISHIMOTO C.
 PA (TOYJ) TOSOH CORP.
 XX
 DR WPI; 1993-161739/20.
 DR N-PSDB; AAQ41746.
 XX
 PT New interleukin-6 receptor deriv. - for treating diseases caused
 by IL-6, e.g. multiple myeloma

Disclosure; Page 10-12; 23pp; Japanese.
 XX
 CC This sequence represents an interleukin-6 (IL-6) receptor. Variants
 CC of the receptor lacking either the immunoglobulin-like domain or the
 CC transmembrane and intracellular domain have IL-6 binding ability and
 CC signal transfer ability. Either the full length or truncated IL-6
 CC receptors may be used for diseases caused by IL-6 such as multiple
 CC myeloma.
 XX
 SQ Sequence 468 AA;

Query Match 16.1%; Score 367.5; DB 14; Length 468;
 Best Local Similarity 28.4%; Pred. No. 8.7e-18;
 Matches 129; Conservative 56; Mismatches 198; Indels 71; Gaps 18;

QY 1 MSSSGLSRLVAVATALVSASPCQAWPGPGVOYGGPGRSVKLCPCGVTAGD--PVS 58
 Db 2 lavgcallaallaapgaal--aprrcpagvavrgvitslpdgsdvtlcpvpednatvh 59
 QY 59 WFRDGEPLKLOGPD-----SGLGHELVLAQADSTDECTYICQTLIDGALGCTVTILQIG 110
 Db 60 w-----virkpaagshpsrwagmrrllrsvqlhdsgnyscyra-grpagtvlhld 111

QY 111 YPPARVWSC-QAADYENFSCWSPSQISGLPTRYLTSTYRKKTVLGADSORRSPSTG-PW 168
 Db 112 vpbeeqblscfrksplsnvvcwgrstpsltt-----kavllvrkfqnspaedfge 163
 QY 169 PC----PQDPLGAARCVVHGAEFWSOYRINVTENVPLGGASTRLLDVSLQSIILRPDPPOG 224
 Db 164 pcqysesqkfsqqlavpegds--sfyivmcvassvgsksftqtfgcgilqdpdpn 221
 QY 225 LRVESYPGYPRGLRASWTYPASWPCQPHFLKFLPQYRPAQHPAWSTVEPAGLEE--VIT 282
 Db 222 itvtavarnprwlsvtwqphsw-n-ssfyrlrfelyraersktfttmvkdqlqhcvh 280
 QY 283 DAVAGLPHAVRSARDFLDAGTWTSTWSPAWGTPSTGTIPKEIPAWGQLHTQPEVEPQVD 342
 Db 281 dawsglrhvvtqlraeqefggewsewseamgtptwtes-----rspaenevs 328
 QY 343 SPAPPRPSLOPHRLDHRDSVEQVAV-----LASLGILSFLGLVAGALALG----- 389
 Db 329 tpmqalttkddnll-frdsanatslpvqdsstsvlptfl-vagsglafgtllciaivl 386
 QY 390 ----LW-LRLRRGGKDGSPKPGFLASVIPVDRRP 418
 Db 387 rfkktwklralkegktsmhpypslgqlvperprp 420

RESULT 14
 AAB36655
 ID AAB36655 standard; Protein; 468 AA.
 XX
 AC AAB36655;
 XX
 DE 13-MAR-2001 (first entry)
 XX
 KW Human IL-6 receptor subunit alpha protein SEQ ID NO:12.
 KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
 KW modulating cell proliferation; diagnosis; detection; drug screening;
 KW immunological disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200073451-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAY-2000; 2000WO-US14867.
 XX
 PR 01-JUN-1999; 99US-0322913.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
 XX
 DR WPI; 2001-061536/07.
 XX
 PT Novel composition comprising DNAX cytokine receptor subunit polypeptide
 PT useful for regulating immune system function and for treating
 PT immunological disorders
 XX
 XX Disclosure; Page 13-15; 93pp; English.
 XX
 CC The present invention describes a composition (I) comprising a
 CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
 CC The DCRS2 polypeptide is useful for binding ligands and for preparing
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
 CC proliferation, for diagnostic and therapeutic applications, for
 CC detecting presence of their ligands and in drug screening assays. It
 CC is also useful for treating conditions such as immunological disorders.
 CC The present sequence represents a cytokine receptor subunit protein
 CC which is given in an alignment of various cytokine receptor subunits in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 468 AA;

```

Query Match      16.1%; Score 367.5; DB 22; Length 468;
Best Local Similarity 28.4%; Pred. No. 8.7e-18;
Matches 129; Conservative 56; Mismatches 198; Indels 71; Gaps 18;

QY 1 MSSSGSLSRVLAVAVATLVASASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGD--PVS 58
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 2 lavgcallaallaagaal--aprrcpaqevargvltslpdsvtlpcgvepednatvh 59
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 59 WFRDGEPLKLOGPD-----SGLGHELVLAQADSTDEGTICQTLQALGGTVTLQLG 110
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 60 w-----vLrkpaagshpsrwagmrrllrsqvlhdsngyscyra-grpagtvlhllvd 111
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 111 YPPARPVVSC-QAADYENFSCWTSQISGLTPRLTYLTSYRKKTVLGADSQRRSPSTG-PW 168
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 112 vppeeqiscfrkspklsnvvcwgrprstpsltt-----kavllvrkfgspaedfge 163
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 169 PC----PODPLGAARCVVHGAEFWQYRINVTENVNPLGAGSTRLLDVSLSQSLRDPDPQG 224
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 164 pcqysqesqkfcqlavpegds--sfyivmcvassvsgskfktqtfqgcgilqdpdpnan 221
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 225 LRVESVGPYPRGLRASWTYPASWPCOPHLLKFRLOYRPAQHAWSTVEPAGLEE--VIT 282
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 222 itvtavarnprwlsvtwqphswn--ssfyrlrfelryraersktfttmvkdqlghcvih 280
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 283 DAVAGLPHAVRYSAARDFLDAGTWSTWSPWAGTTPGTIPKEIPAWGOLHTQPEVEPQVD 342
   ||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 281 dawsglrhvvgqlraeeefgqgsewseamgtpwtes-----rspgaenevs 328
   ||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 343 SPAPPRPSLQHPRLDHRDSVEQVAV-----LASLGILSFLGLVAGALALG----- 389
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 329 tpmqalttnkddnll-frdsenatslpvqsdssvplptfl-vagsglafgtllciaiavl 386
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 390 ----LW-LRLRGGKDGSPKPCFLASVIPVDRRP 418
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 387 rfkktwkrlalkegktsmhppyslgqlvperprp 420
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 15
AAR20024
ID AAR20024 standard; Protein; 372 AA.
XX AC AAR20024;
XX DT 31-MAR-1992 (first entry)
XX OS Ciliary neurotrophic factor receptor.

CNTFR; transgenic animal; motoneurone disease; trauma;
muscular dystrophy; inflammation; amyotrophic lateral sclerosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 42..90
XX FT /note= "Ig-like"
XX FT Domain 116..294
XX FT /note= "cytokine receptor-like "
XX PN W09119009-A.
XX PD 12-DEC-1991.
XX PF 03-JUN-1991; 91WO-US03896.
XX PR 15-MAY-1991; 91US-0700677.
XX PR 01-JUN-1990; 90US-0532285.
XX PR 28-MAR-1991; 91US-0676647.
XX PA (REGE-) REGENERON PHARM INC.
XX PI Davis S, Squinto S, Furth M, Yancopoulos GD;
```

```

XX WPI: 1992-007490/01.
DR N-PSDB: AAQ20195.
XX DNA encoding CNTF receptors - useful in diagnosis, physiological
PT study and treatment of CNTF-related disorders
XX Claim 16; Fig 2; 92pp; English.
XX The CNTFR has an Ig-like domain fused to the N-terminus of the
CC proposed factor binding domain via a short acidic tether. The
CC protein is structurally similar to IL-6 receptor.
XX Sequence 372 AA;

Query Match      16.1%; Score 366.5; DB 13; Length 372;
Best Local Similarity 30.0%; Pred. No. 7.8e-18;
Matches 122; Conservative 47; Mismatches 168; Indels 69; Gaps 16;

QY 12 LVAVATLVASASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWFRDGEPLKLOGP 71
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 12 vlaaaaavvyqrhspqe--aphvgyerlgsdvtlpcgtanwdaavtrvngtd---lap 66
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 72 DSGLGHELVLAQADSTDEGTICQTLDG--ALGCTVTLQLGYPARPVVSQAADY--ENFS 129
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 67 dlilngsqvlhglelghsglyacfhrrdswlhrhqvllhvglpprepviscrantypkgfy 126
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 130 CTWSPSQISGLPT-RYLTSYRKKTVLGADSQRRSPSTGFWPCQDPLGAARCVVHGAEFW 188
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 127 cswh-----lptptyipntfnvtvlhgsk-----lmvcekdpalknchrchymhlf 172
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 189 S--QYRINVTENVNPLGAGSTRLLDVSLSQILRPDPQGLRVESVPGYPRGLRASWTYPAS 246
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 173 stikykvsvsivsnalghnataitfdef-tlvkdpdpennvvarpvpsnprlvtwtqst 231
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 247 WPCQPHLLKFRLOYRPAQHAWSTVEPA-GLEEYITDAVAGLPHAVRYSAARDFLDAGTW 305
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 232 wdpesfplkflryrplldqwhveisdgtahitdayagkeyliqvaaakd-neigtw 290
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 306 STWSPWANGTPTGTIPKEIPAWGOLHTQPEVEPQVDSPAPPRPSLQHPRLDHRDSVE 365
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 291 sdwsvaahatpwtee-prhlhtteaq--aaettststslapp-----pttkicd----- 336
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 366 QVAVLASLGILSFLGLVAGALALGLWLRGGKDGSPKPCFLASV 411
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 337 -----ppql-----gsgggpcapflvsv 354
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

Search completed: August 24, 2001, 17:32:31
Job time: 114 sec

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO) _____


```

Db 149 RNMKDUTCRWTPGAHGETLHTNYSKYLRLWYQDNTCEEYHTVGPCHSHPKD----- 203
QY 179 RCVVHGAERWQYRINVTENPLGGASTRLLDVSLQSLRPPDPCGLRVESVPGYPRGLR 238
Db 204 -----LALFTPEIWEATNRLGARSVDLVLVDVTTDPPDVHVSRLVGGLEDQLS 257
QY 239 ASWTYPASWPCQPHFL--KFLQYRPAQHPAWSTYEP-----AGLEEVITDAVAG 287
Db 258 VRWVSP---PALKDFEQAQYQIRYRVEDSVDMKVVDVSNQTSCLAGLK-----PG 307
QY 288 LPHAVRVSARDP-----LDAGTWSTWS-PEA-----WGTPSTGTTP 322
Db 308 TVYFVQVRNPGFIYSGKAGIWSHSEHTAASPRSGPGGGVCEPRGGPSSGPRV 367
QY 323 KEIP---AWGOLH 332
Db 368 RELKQFLGLKXH 380

RESULT 12
O46561 PRELIMINARY; PRT: 581 AA
AC O46561: P79205; O46574; P79203; O46569;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (PRLR) (OPR).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=HAMMARY GLAND, AND LIVER;
RX MEDLINE=98001468; PubMed=9343303;
RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
RT and genomic analysis reveal that the two forms arise by different
RT alternative splicing mechanisms in ruminants and in rodents.";
RT J. Mol. Endocrinol. 19:109-120(1997).
RN [2]
RP SEQUENCE OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=SCOTTISH BLACKFACE / ISOLATE M22/80; TISSUE=ANTERIOR PITUITARY;
RX MEDLINE=99049302; PubMed=9832462;
RA Tortorese D.J., Brooks J., Ingletton P.M., McNeilly A.S.;
RT "Detection of prolactin receptor gene expression in the sheep
RT pituitary gland and visualization of the specific translation of the
RT signal in gonadotrophs.";
RT Endocrinology 139:5215-5223(1998).
RN [3]
RP SEQUENCE OF 147-302 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=FETAL LIVER, AND CORPUS LUTEUM;
RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;
RT "Two forms of the prolactin receptor messenger ribonucleic acid are
RT present in ovine fetal liver and adult ovary.";
RT Endocrine 3:291-295(1995).
RN [4]
RP FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS; LONG ISOFORM (L-OPR) (SHOWN
CC HERE), SHORT ISOFORM (S-OPR) AND SOLUBLE ISOFORM; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (LIVER,
CC PITUITARY, ADRENAL GLAND, OVARY AND FETAL LIVER).
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL: AF041257; AAB96795.1; -
DR EMBL: AF041977; AAB96920.1; -
DR EMBL: AF041979; AAB97082.1; -
DR EMBL: AF042358; AAB97744.1; -
DR EMBL: AF042358; AAB97743.1; -

```

```

DR EMBL: AF041978; AAB96965.1; -
DR EMBL: Y10578; CAA71597.1; -
DR EMBL: Y10808; CAA71766.1; -
DR HSSP: P14787; IAN3.
DR InterPro: IPR001777; -
DR InterPro: IPR002996; -
DR InterPro: IPR003528; -
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 237
FT TRANSMEM 238 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT VARSPLIC 24 66
FT VARSPLIC 67 581
FT VARSPLIC 286 296
FT VARSPLIC 297 581
FT CONFLICT 281 281
FT CONFLICT 387 387
FT SEQUENCE 581 AA; 65235 MW; EC534FDE538837A0 CRC64;
SQ
Query Match 9.3%; Score 212; DB 6; Length 581;
Best Local Similarity 26.8%; Pred. No. 2.5e-08;
Matches 61; Conservative 35; Mismatches 96; Indels 36; Gaps 9;
QY 112 PPARP-VVSCQAADYENFSCVSPQISGLPTRYLTYSRKKTVLGDASQRRSPSTGFWC 170
DB 27 PPEKPKLKRSPGKETFTCWEPGAGGLPTNYTYRKE-----GETLIHCC 75
QY 171 PQDPLGAACVHVHGADEF---WSQYRINVTENPGLGASTRLLDVSLQSLRPPDGLRV 227
DB 76 PDYKGGPNSCVFSKXYTSIWKMYVITVSAIQMGLSSSDPLYVDVYIVVEPPNNLTL 135
QY 228 ESWPGYPRG--LRASWYTP-----ASWPCQPHFLKFLQYRPAQHPAWST--VEPAGE 278
DB 136 ELKHEDRKPYLWIKWSPPTLTDVKSQW-----FSIQYEIRLKPKEKATDWTHTFAPKLQ 190
QY 279 EVITDAVAGLPHAVRVSARDPDLDAWTWSPEAWGTPSTGTIPKEIP 326
DB 191 LKIFNLPQGYLVQIRCKP--DHGYWSEWSPE-----SFIQIPNDPF 231
RESULT 13
O18880 PRELIMINARY; PRT: 296 AA.
AC O18880;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97375450; PubMed=9231767;
RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;

```



```

DR HSP; P40189; 180U.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT CHAIN 37
FT SIGNAL 38
SQ SEQUENCE 422 AA; 46301 MW; AD9DFCB01B84228 CRC64;

Query Match 9.6%; Score 219; DB 4; Length 422;
Best Local Similarity 23.7%; Pred. No. 51e-09;
Matches 91; Conservative 52; Mismatches 147; Indels 94; Gaps 18;

QY 7 GLSRVLVAVAVATVAVSASSPCQAWPGVQVQPCGRSVKLCG-----PGVTAGDPVSWF 60
DB 30 GAPRAGSAGHTAVISPDPTLLI-----GSSLLATCSVHGDDPPGATA-EGLYWT 77
QY 61 RDGE---PKLLQGPDSGLGHELVLAQAD-----STDEGTIICOTLDGALGGTIVTLQLGYP 112
DB 78 LNGRRLPELSRVLNAS---TLALALANLNGSRQSGDNLVCHARDGSSILAGSCLYVGLP 134
QY 113 PARPV-VSCQAADYENFSCWTSPSQ--ISGLPTRYLTYSRKTKTVLGADSORRSPSTGWP 169
DB 135 PEKPNINISCSWKNMDDLRCRTWPGAHGETFLHTNYSKYKLRWYGODNTCEEYHTVGP 194
QY 170 C--PODPLGAARCVVHGAFFWSOYRINVTENPLGGASTRLLDVLSLOSLTLRPDQGLRV 227
DB 195 CHIPKD-----LALFTPYEIWEATNRLGARSDDLTLDDVVTDTDPDPVHV 243
QY 228 ESVGPGYRGLRASWTYPASWPCQPHLL--KRLQYRPAQHPAWSTVEP-----AG 276
DB 244 SRVGGLEDQLSVRWVSP---PALKDFLQAKYQIRYVEDSVDMKVDDVDSNOTSCRLAG 300
QY 277 LEEVITDAVAGLPHAVRVSARDF-----LDAGTWTWS-PEA-----312
DB 301 LK-----PGTVFVQVRCNPFGIYGSKKAGINSEWSHPTAASPRSERPGPGGGACEP 353
QY 313 -WGTPSTGTIPEIP---AWGOLH 332
DB 354 RGEFSSGVRRELKQFLGWLKKH 377

RESULT 10
Q9UHH5 PRELIMINARY; PRT; 422 AA.
ID Q9UHH5
AC Q9UHH5
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jernberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178684; AAD54385.1; -.
DR HSP; P40189; 180U.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 9.6%; Score 218; DB 4; Length 422;

```

```

Best Local Similarity 23.7%; Pred. No. 6e-09;
Matches 91; Conservative 52; Mismatches 147; Indels 94; Gaps 18;

QY 7 GLSRVLVAVAVATVAVSASSPCQAWPGVQVQPCGRSVKLCG-----PGVTAGDPVSWF 60
DB 30 GAPRAGSAGHTAVISPDPTLLI-----GSSLLATCSVHGDDPPGATA-EGLYWT 77
QY 61 RDGE---PKLLQGPDSGLGHELVLAQAD-----STDEGTIICOTLDGALGGTIVTLQLGYP 112
DB 78 LNGRRLPELSRVLNAS---TLALALANLNGSRQSGDNLVCHARDGSSILAGSCLYVGLP 134
QY 113 PARPV-VSCQAADYENFSCWTSPSQ--ISGLPTRYLTYSRKTKTVLGADSORRSPSTGWP 169
DB 135 PEKPNINISCSWKNMDDLRCRTWPGAHGETFLHTNYSKYKLRWYGODNTCEEYHTVGP 194
QY 170 C--PODPLGAARCVVHGAFFWSOYRINVTENPLGGASTRLLDVLSLOSLTLRPDQGLRV 227
DB 195 CHIPKD-----LALFTPYEIWEATNRLGARSDDLTLDDVVTDTDPDPVHV 243
QY 228 ESVGPGYRGLRASWTYPASWPCQPHLL--KRLQYRPAQHPAWSTVEP-----AG 276
DB 244 SRVGGLEDQLSVRWVSP---PALKDFLQAKYQIRYVEDSVDMKVDDVDSNOTSCRLAG 300
QY 277 LEEVITDAVAGLPHAVRVSARDF-----LDAGTWTWS-PEA-----312
DB 301 LK-----PGTVFVQVRCNPFGIYGSKKAGINSEWSHPTAASPRSERPGPGGGACEP 353
QY 313 -WGTPSTGTIPEIP---AWGOLH 332
DB 354 RGEFSSGVRRELKQFLGWLKKH 377

RESULT 11
Q9JMS8 PRELIMINARY; PRT; 425 AA.
ID Q9JMS8
AC Q9JMS8
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.
GN CRLM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040038; BAA92777.1; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL 34
FT SIGNAL 34
SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 9.5%; Score 217; DB 11; Length 425;
Best Local Similarity 23.9%; Pred. No. 7.3e-09;
Matches 89; Conservative 52; Mismatches 140; Indels 92; Gaps 17;

QY 17 TALVSASSPCQAWPGVQVQPCGRSVKLCG-----PGVTAGDPVSWFRDGEKLLQ 70
DB 43 TAVISPDPTLLI-----GSSLOATCSIHGDTPGATA-EGLYWTNG--RRLPS 88
QY 71 PDSGLGHELVLAQADSTDEGT-----YICQTLGALGGTIVTLQLGYPVPPARV-VSCOA 122
DB 89 ELSRLNTSTALANLNGSRQSGDNLVCHARDGSSILAGSCLYVGLPPEKPFNISCWS 148
QY 123 ADYENFSCWTSPSQ--ISGLPTRYLTYSRKTKTVLGADSORRSPSTGWPWC--PODPLGAA 178

```

```
RESULT 7
Q14213
ID Q14213 PRELIMINARY; PRT; 229 AA.
AC Q14213;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR PRECURSOR.
GN EBI3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96135230; PubMed=8551575;
RA Devergne O., Hummel M., Koepfen H., Le Beau M.M., Nathanson E.C.,
RA Kieff E., Birkenbach M.;
RT "A novel interleukin-12 p40-related protein induced by latent Epstein-
RT Barr virus infection in B lymphocytes.";
RL J. Virol. 70:1143-1153(1996).
DR EMBL; L08187; AAA93193.1; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 229 CYTOKINE RECEPTOR.
SQ SEQUENCE 229 AA; 25391 MW; F42875A4815D81C7 CRC64;

Query Match 10.7%; Score 244; DB 4; Length 229;
Best Local Similarity 30.8%; Pred. No. 3.2e-11;
Matches 73; Conservative 35; Mismatches 95; Indels 34; Gaps 11;

QY 94 CPTLDGALGGTTLQLGYPPAR---PWSCOAADYE-NFSCWTS---PSQISGLPTRYLTS 147
DB 15 CPPCSRKG-----PPAALTLPVQCRASRYFIANDCSWLPAPNSPSPVFSFIAT 65
QY 148 YRKKTVLGADSQRRSPSTGPWCPQDPLGAARCVVHGAEFWSQ--YRINVTENPLGGAS 205
DB 66 YR---LGMAARHS-----WPCLQQTPTSTCTITDVLFSMAPVVLNVTAHPWGSSS 116
QY 206 TRLLDVSLSQILRPDPQGLRVESVPGYPRGLRASWTYPASWPCQPHFLKFLQYRPAQ 265
DB 117 S-FVPTFITEHIKDPPEGVRLS--PLAERHVQVQVQWEPFGSNWPFPEIFSLKYWIRYKROG 173
QY 266 HPAMSTVEPAGLEEVITDAVAGLPHA---VRVSARDFLDAGTWSTWSPAWGTPSTG 319
DB 174 AARFHRVGPIEATSFILRAVR--PRARYVQVAQQDLTDYGLSDWSLPATATMSLG 228

RESULT 8
O57519
ID O57519 PRELIMINARY; PRT; 881 AA.
AC O57519;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE GP130P1.
DE GP130P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
```

```
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC03531.1; -.
DR HSPB; P40189; 1BQU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003529; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138AC CRC64;

Query Match 9.8%; Score 223; DB 13; Length 881;
Best Local Similarity 23.3%; Pred. No. 5.7e-09;
Matches 88; Conservative 61; Mismatches 146; Indels 82; Gaps 18;

QY 1 MSSSCSLSRVLVAVATALVSASSPCPAWPGVQYQGPCRSVKLCCPCGVT A----GDP 56
DB 5 ISFFCLISSVVLIVHOAELVKV---CGRIFFDPGIVHGERPETA-YCVINQTCREDASR 60
QY 57 VSMFRDG-----EPKLLOGPDSGLGHELVLAQADSTDEGTVICQTL-DGALGGT---VT 106
DB 61 IYWLKGVKVPETOYEILNQTTSSVTFENL-----TTLASPLTCNVMSHVAANTLYGIF 115
QY 107 LQLGYPPARPV-VSCQAADYENFSCWTSQISGLPRVLTYSYRKKTVLGADSQRRSPST 165
DB 116 FTGLPDPKPTNLTCIVYNODNLCTWDCGRPTNLPTNTVLTSLR-WAHEGANCYRGANNS 174
QY 166 GWPCCPDPLGAARCVVH--GAEFWSQYRINVTENPVLGAGSTRLLDVSLOSILRDPQPQ 223
DB 175 -----CTIHSFGFYIDTTFQVEATRELGIQKSETLTIDPVNIVKPNPQ 220
QY 224 GLRVESVPGYPRGLRASWTYPASWPCQPHFLKFLQYRPAOHPAWSTV-----EP 274
DB 221 LSELISLLEPLNALKIEWKNPIT---NAFNLYNRYRPVKTDQWEMPEEDTASHRDS 276
QY 275 AGLEEIVTDAVAGLPHAVRSARDFLDAGTWSTWS-----PEAWGTPSTGTIPKEIPA 327
DB 277 FTQLDQLLNPVTVEV--SIRCIHKD--GHGFWSDWSLKKQVTPEA--PPSRG----- 322
QY 328 WQQLHTQPEVEQVDSF 344
DB 323 -----PDIWKKIDSP 332

RESULT 9
O75462
ID O75462 PRELIMINARY; PRT; 422 AA.
AC O75462;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-I Receptor Family.";
RL J. Immunol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hematopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059293; AAC28335.1; -.
DR EMBL; AF073515; AAD39681.1; -.
```

```
DR InterPro: IPR003530; -.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; ig; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW SIGNAL.
FT SIGNAL. 1 20 POTENTIAL.
FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT CHAIN 21 336 ALPHA.
SQ SEQUENCE 372 AA; 40831 MW; EB75A9EE6A1BB8C8 CRC64;

Query Match 16.4%; Score 373.5; DB 11; Length 372;
Best Local Similarity 31.5%; Pred. No. 7e-21;
Matches 112; Conservative 49; Mismatches 164; Indels 31; Gaps 13;

QY 1 MSSSCGLSRVLAVATALVSASSPCPAWPGVQYQGRSVKLCPCGVTAGDPVSWF 60
DB 1 MTASVPWACCAVLAANAAYTKKISQOE--APHVOYERLGADVTLPCCGTASWDAAVTWR 58
QY 61 RDGEPLKLGQDGLGHELVLAQADSTDEGTICQTLDG-ALGGTVTLQLGYPARPVVS 119
DB 59 VNGTD--LAPDLLNGSQLILRLSLGLSHGLYACFHRDSWHLRHQVLLHVGLPPREPVL 115
QY 120 QQAADY-ENFSTWSPSQISGLPT-RYTSYRKTKVLGADSORRSFSTGWPCCPODPLGA 177
DB 116 CSRNTYPRGFGYSW------LPTPTYPNTFNVTVLHGSK-----IMVCKDKPALK 161
QY 178 ARCVVHGAEFNS--CYRINVTENVPLGCASTRLLDVLSQSLRPPQGLRVESVPGYPR 235
DB 162 NCCHRYWHLFSTIKYKVISISVSNAL-GHNTTATTFDEFTIVKPPDENVVARPPSNPR 220
QY 236 GLRASWTYPASWPCOPHFLKFRLOYRAQHPAWSTVEPA-GLEEVITDAVAGLPHAVRV 294
DB 221 RLEVWQPTSTWPDSPESPLKEFLRYRLILDQWQHVELSDGTAHTIDAYAGKEYITQV 280
QY 295 SARDELDAGTWSPEAWGTPTSTGTPKEIPAWQSLHTQPEVQVDSPPAPRPS 350
DB 281 AAKD-NEIGTWSWNSVAHAATPWTEE-PRHLTTEAQ---APETTTTSTSSSLAPPPT 331

RESULT 5
ID O35228 PRELIMINARY; PRT; 228 AA.
AC O35228;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR-LIKE MOLECULE.
GN EBT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Nomura H., Yaguchi N., Hanyuu C., Maeda M., Kikuchi Y., Nakata Y.,
RA Kojima T., Tulin E.E., Hasegawa M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF013114; AAB67115.1; -.
DR MGD: MGI:135417; EBI3.
DR InterPro: IPR000282; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003530; -.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
SQ SEQUENCE 228 AA; 25353 MW; 49DEFA4E5C4F2126 CRC64;

Query Match 11.5%; Score 261.5; DB 11; Length 228;
Best Local Similarity 35.3%; Pred. No. 1.4e-12;
Matches 74; Conservative 34; Mismatches 95; Indels 34; Gaps 11;
```

```
Matches 72; Conservative 33; Mismatches 76; Indels 23; Gaps 9;

QY 114 ARPVSCQAADYE-NFSCTWSPSQI--SGLPTRYLTSYRKTKVLGADSORRSFSTGWPCC 170
DB 28 SOPRVQCHASRYPPVAVDCSWTLPQAPNSTRSFTATYR----LGVATQOQSQ-----PC 78
QY 171 PODPLGAARCVVHGAEFNS--QYRINVTENVPLGCASTRLLDVLSQSLRPPQGLRV 228
DB 79 LQSPQASRCTIPDVHLFSTVPYMLNVTAVHP-GGASSLLAFVAERIITKPPPEGVRLR 137
QY 229 SVPGYPRGLRASWTYPASWPCOPHFLKFRLOYRAQHPAWSTVEPAGLEEVITDAVAGL 288
DB 138 TA---GQRLQVLWHPASPMPFDDIFSLKRLYRRRGASHFRQVGP--IEATFTLRNSK 192
QY 289 PHA---VRVSARDELDAGTWS 309
DB 193 PHAKYCIQVSAQDLTDYKPKSDWS 216

RESULT 6
ID O75269 PRELIMINARY; PRT; 229 AA.
AC O75269;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE HUMAN CYTOKINE RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lanerding J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco M., Do L., Regala W., Terry A., Gaines J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL "Sequence analysis of a 2.5 Mb region in 19p13.3.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC005578; AAC33488.1; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003530; -.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
SQ SEQUENCE 229 AA; 25396 MW; CFBAD72D91859EF0 CRC64;

Query Match 10.8%; Score 247; DB 4; Length 229;
Best Local Similarity 31.2%; Pred. No. 1.9e-11;
Matches 74; Conservative 34; Mismatches 95; Indels 34; Gaps 11;

QY 94 CQTLGALGGTTLQLGYPAR---PVVSCQAADYE-NFSCTWSPSQISGLPTRYLTS 147
DB 15 CPCSGRKG-----PPAALTLPVOCRASRPPIAVDCSWTLPAPNSTRSFVFIAT 65
QY 148 YRKTKVLGADSORRSFSTGWPCCQDPLGAARCVVHGAEFNSQ---YRINVTENVPLGAS 205
DB 66 YR----LGMAARGHS-----WPCLOQTPTSTCTITDVOLFSPMAPVVLNVTAVHPWGS 116
QY 206 TRLLDVLSQSLRPPQGLRVESVPGYPRGLRASWTYPASWPCOPHFLKFRLOYRPAQ 265
DB 117 S-FVPFITEHIKPPPEGVRLS--PLAERQLQVQMEPPGSPFPFEISLKYIRKRG 173
QY 266 HPASTVTEPAGLEEVITDAVAGLPHA---VRVSARDELDAGTWSPEAWCTPTSG 319
DB 174 AARHVRVPIEATSFILRAVR--PRARYVQVAADLTQDYGELSDWSLPAATYNSLG 228
```


DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART; SM0060; FN3; 1.
SQ SEQUENCE 422 AA; 45222 MW; 1F8BC05C139FC326 CRC64;

Query Match 98.9%; Score 2257.5; DB 4; Length 422;
Best Local Similarity 99.5%; Pred. No. 1.1e-164;
Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MSSSCSGLSRVLAVATLVASSPCPAWGPVQYQGPGRSVKLCPCGVTAGDPVSWF 60
Db 1 MSSSCSGLSRVLAVATLVASSPCPAWGPVQYQGPGRSVKLCPCGVTAGDPVSWF 60
QY 61 RDGEPLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVYSC 120
Db 61 RDGEPLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVYSC 120
QY 121 QAADYENFSCWSPSQISGLPTRYLTYSRKKTVLGADSORRSPSTGMPCPQDPLGAARC 180
Db 121 QAADYENFSCWSPSQISGLPTRYLTYSRKKTVLGADSORRSPSTGMPCPQDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENPLGGASTRLLDVLSQILRPDPQGLRVESVPGYPRGLRAS 240
Db 181 VVHGAEFWSQYRINVTENPLGGASTRLLDVLSQILRPDPQGLRVESVPGYPRGLRAS 240
QY 241 WTYPASWPCQHPFLKFRLOYRPAQHPAWSITVEPAGLEEVITDAVAGLPHAVRVARSDFL 300
Db 241 WTYPASWPCQHPFLKFRLOYRPAQHPAWSITVEPAGLEEVITDAVAGLPHAVRVARSDFL 300
QY 301 DAGTWTSTWSPANGTPTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLOPHRLLDH 360
Db 301 DAGTWTSTWSPANGTPTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLOPHRLLDH 360
QY 361 RDSVEQVAVLASGLISLGLVAGALGLWLRGKDGSPKPGFLASVLPVDRRPGA 420
Db 361 RDSVEQVAVLASGLISLGLVAGALGLWLRGKDGSPKPGFLASVLPVDRRPGA 420
QY 421 PNL 423
Db 420 PNL 422

RESULT 2
Q64385 PRELIMINARY; PRT; 432 AA.
AC Q64385;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
DE (IL-11RALPHA) (IL11RAL).
GN IL11RAL OR IL11RA OR ETL2 OR ETL12/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE=95045367; PubMed=7957045;
RA Hilton D.J., Hilton A.A., Raicevic A., Rakar S., Harrison-Smith M.,
RA Gough N.M., Begley C.G., Metcalf D., Nicola N.A., Willson T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130
for high affinity binding and signal transduction.";
RL EMBO J. 13:4765-4775(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6; TISSUE=EMBRYO;
RA Neuhaus H., Bettenhausen B., Billinski P., Simon-Chazottes D.,
RA Guenet J.L., Gossler A.;
RL Dev. Biol. 166:521-542(1994).
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6;
RA Gossler A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97129000; PubMed=8973540;
RA Billinski P., Hall M.A., Neuhaus H., Gissel C., Heath J.K., Gossler A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
mouse genome.";
RL Biochem. J. 320:359-363(1996).
CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11. BINDS TO IL-11
WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE IG-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC EMBL; X74953; CAA52908.1; -;
DR EMBL; U14412; AAA53248.1; -;
DR EMBL; X94162; CAA63873.1; -;
DR EMBL; X94163; CAA63873.1; JOINED.
DR MGI; I07426; Il11ral.
DR InterPro; IPR001777; -;
DR InterPro; IPR002996; -;
DR InterPro; IPR003006; -;
DR InterPro; IPR003530; -;
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART; SM0060; FN3; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 23
FT CHAIN 24 432
FT DOMAIN 24 367
FT TRANSMEM 368 393
FT DOMAIN 394 432
FT DOMAIN 41 102
FT CARBOHYD 127 127
FT CARBOHYD 194 194
SQ SEQUENCE 432 AA; 46655 MW; 068389943502BBFC CRC64;

Query Match 82.4%; Score 1879.5; DB 11; Length 432;
Best Local Similarity 83.1%; Pred. No. 8.1e-135;
Matches 353; Conservative 18; Mismatches 51; Indels 3; Gaps 2;

QY 1 MSSSCSGLSRVLAVATLVASSPCPAWGPVQYQGPGRSVKLCPCGVTAGDPVSWF 60
Db 1 MSSSCSGLTRVLAVATLVASSPCPAWGPVQYQGPGRSVKLCPCGVTAGDPVSWF 60
QY 61 RDGEPLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVYSC 120
Db 61 RDGEPLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVYSC 120
QY 121 QAADYENFSCWSPSQISGLPTRYLTYSRKKTVLGADSORRSPSTGMPCPQDPLGAARC 180
Db 121 QAADYENFSCWSPSQISGLPTRYLTYSRKKTVLGADSORRSPSTGMPCPQDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENPLGGASTRLLDVLSQILRPDPQGLRVESVPGYPRGLRAS 240
Db 181 VVHGAEFWSQYRINVTENPLGGASTRLLDVLSQILRPDPQGLRVESVPGYPRGLRAS 240
QY 241 WTYPASWPCQHPFLKFRLOYRPAQHPAWSITVEPAGLEEVITDAVAGLPHAVRVARSDFL 300
Db 240 WTYPASWRRQHPFLKFRLOYRPAQHPAWSITVEPAGLEEVITDAVAGLPHAVRVARSDFL 299
QY 301 DAGTWTSTWSPANGTPTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLOPHRLLDH 360
Db 300 DAGTWTSTWSPANGTPTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLOPHRLLDH 359
QY 359 DHRDSVEQVAVLASGLISLGLVAGALGLWLRGKDGSPKPGFLASVLPVDRRP 418

GenCore version 4.5

Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2001, 17:34:11 ; Search time 37.87 Seconds
(without alignments)
1477.820 Million cell updates/sec

Title: US-09-532-263-5

Perfect score: 2282

Sequence: 1 MSSCSGLSRVLVAVATLV.....KPGFLASVIVDRRPGAPNL 423

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL16.*

1: sp-archaea.*

2: sp-bacteria.*

3: sp-fungi.*

4: sp-human.*

5: sp-invertebrate.*

6: sp-mammal.*

7: sp-mhc.*

8: sp-organelle.*

9: sp-phage.*

10: sp-plant.*

11: sp-rodent.*

12: sp-unclassified.*

13: sp-vertebrate.*

14: sp-virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2257.5	98.9	422	4	Q16542 homo sapien
2	1879.5	82.4	432	11	Q64385 mus musculus
3	1853.5	81.2	432	11	P70225 mus musculus
4	373.5	16.4	372	11	O88507 mus musculus
5	261.5	11.5	228	11	O35228 mus musculus
6	247	10.8	229	4	O75269 mus sapien
7	244	10.7	229	4	Q14213 homo sapien
8	223	9.8	881	13	O57519 xenopus lae
9	219	9.6	422	4	O75462 homo sapien
10	218	9.6	422	4	Q90UH5
11	217	9.5	425	11	Q9JTM58
12	212	9.3	581	6	O46561 ovis aries
13	207	9.1	296	6	O18880 bos taurus
14	195	8.5	611	13	Q9PTH9
15	191.5	8.4	227	6	Q9GLW3
16	191.5	8.4	346	13	O93404
17	191	8.4	206	4	Q16354
18	190	8.3	611	13	Q9PTIO
19	190	8.3	611	13	Q9IBF6

20	189.5	8.3	349	4	Q9UJH5
21	189	8.3	538	13	Q9DFU0
22	186	8.2	625	6	Q9X592
23	184.5	8.1	622	6	Q9NOJ7
24	182.5	8.0	327	11	Q9ET05
25	179.5	7.9	327	6	Q9TT18
26	179.5	7.9	638	13	Q9DE08
27	170	7.4	918	13	Q9W6U9
28	170	7.4	1280	13	Q90933
29	160	7.0	198	6	O18985
30	160	7.0	600	13	Q9PTP0
31	159	7.0	217	6	O46386
32	153.5	6.7	1256	11	Q9ET59
33	152.5	6.7	1242	11	Q9QZS7
34	152.5	6.7	1256	11	Q9JIX1
35	151.5	6.6	1234	11	Q9R044
36	151.5	6.6	1252	11	Q9QXX7
37	151.5	6.6	1252	11	Q9JIX2
38	150	6.6	329	4	Q9OQ41
39	144.5	6.3	1948	4	Q13332
40	138.5	6.1	335	11	Q9R278
41	138.5	6.1	1241	4	O60500
42	138	6.0	1162	11	Q9QWG3
43	138	6.0	1898	11	Q84604
44	138	6.0	1898	11	Q9EQI7
45	137.5	6.0	335	11	Q9QUM1

ALIGNMENTS

RESULT 1

Q16542	PRELIMINARY;	PRT;	422 AA.
AC	Q16542	Q14626;	
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DE	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	INTERLEUKIN-11 RECEPTOR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=MUSCLE;		
RX	MEDLINE=95399754; PubMed=7670098;		
RA	Cherel M., Sorel M., Lebeau B., Dubois S., Moreau J.F., Bataille R.,		
RA	Minvielle S., Jacques Y.;		
RT	"Molecular cloning of two isoforms of a receptor for the human		
RL	hematopoietic cytokine interleukin-11.";		
RL	Blood 86:2534-2540(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Van Leuven F., Stas L., Hilliker C., Miyake Y., Gossler A.;		
RL	Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE OF 3-390 FROM N.A.		
RC	TISSUE=PLACENTA;		
RA	Cherel M., Sorel M., Dubois S., Lebeau B., Moreau J., Jacques Y.,		
RA	Minvielle S.;		
RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
CC	DOMAIN.		
DR	EMBL; U32324; AAB36492.1; -		
DR	EMBL; Z38102; CAA86224.1; -		
DR	EMBL; U32323; AAB36491.1; -		
DR	EMBL; Z46595; CAA86570.1; -		
DR	InterPro; IPR001777; -		
DR	InterPro; IPR002996; -		
DR	InterPro; IPR003006; -		
DR	InterPro; IPR003530; -		
DR	Fram; PF00041; fn3; 2.		

THIS PAGE BLANK (USPTO)


```

CC EMBL; J04510; AAA31457.1; -
DR PIR; A30304; A30304.
DR PDB; 1AN3; 03-DEC-97.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR Pfam; IPR002465; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
FT SIGNAL 1 24 BY SIMILARITY
FT CHAIN 25 616 PROLACTIN RECEPTOR.
FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 258 POTENTIAL.
FT DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
FT DOMAIN 124 227 FIBRONECTIN TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 616 AA; 68840 MW; 800E3166FE7108C CRC64;

Query Match 8.6%; Score 195.5; DB 1; Length 616;
Best Local Similarity 27.3%; Pred. No. 2e-06;
Matches 65; Conservative 28; Mismatches 98; Indels 47; Gaps 13;

QY 112 PPARP-VVSCQADYENFSCWPSQISGLPTRYLSYRKTKVLGADSRSPSTGWPC 170
DB 27 PPGKPIFKRSCEKETFTCWMPRGADGLPTNTLYTHKE-----GETITHEC 75

QY 171 PDPLGAARCVVHG---AEPWSYRINVTENVPLGG--ASTRLLDVSLQILRPDPQGL 225
DB 76 PDYKGTGPNSCYCSKKHTSLWIIYITVNTATNGMSVSDPRVDVY--IVPDPVPNL 133

QY 226 RVESVCPYGRG---LRASWTYP-----ASWPCQPHFLKRLQYRPAQHPAWSTVPAGL 277
DB 134 TLEVHPKEDRKPLWKLWLPPTLVDRSGW-----LTQVEIRLKEPAKEWET-HFAQG 187

QY 278 EE--VTDAVAGLPHAVRSARDELDAQWTSWSPAWGTPTGTTP-----KEIPAW 328
DB 188 QTOFKILSLYPGOKYLQVQRCKP--DHGFWSVMSPE-----SSIQIPNDFMTMKDITVW 238

RESULT 14
PRLR_RAT
ID PRLR_RAT STANDARD; PRT; 610 AA.
AC P05710; Q63451; Q63723; Q62832; Q64274; Q63479;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
GN PRLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE-91155946; PubMed-2293032;
RA Shirota M., Banville D., Ali S., Jolicoeur C., Boutin J.M.,
RA Edery M., Djiane J., Kelly P.A.;
RT "Expression of two forms of prolactin receptor in rat ovary and
RT liver.";
RL Mol. Endocrinol. 4:1136-1143(1990).
[2]
RN SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary;
RX MEDLINE-902411201; PubMed-2159291;
RA Zhang R., Buczek E., Tsai-Morris C.H., Hu Z.Z., Dufau M.L.;
RT "Isolation and characterization of two novel rat ovarian lactogen

```

```

RT receptor cDNA species.";
RL Biochem. Biophys. Res. Commun. 168:415-422(1990).
[3]
RN SEQUENCE OF 281-610 FROM N.A.
RA Banville D., Stocco R., Murthy K.K., Boie Y., Kelly P.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
RP TISSUE=Liver;
RX MEDLINE-88165059; PubMed-2832068;
RA Boutin J.-M., Jolicoeur C., Okamura H., Gagnon J., Edery M.,
RA Shirota M., Banville D., Dusanter-Fourt I., Djiane J., Kelly P.A.;
RT "Cloning and expression of the rat prolactin receptor, a member of
RT the growth hormone/prolactin receptor gene family.";
RL Cell 53:69-77(1988).
[5]
RN SEQUENCE FROM N.A. (FORM NB2).
RP TISSUE=Lymphoma;
RX MEDLINE-92041834; PubMed-1718958;
RA Ali S., Pelligrini I., Kelly P.A.;
RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form
RT of prolactin receptor.";
RL J. Biol. Chem. 266:20110-20117(1991).
[6]
RN SEQUENCE FROM N.A. (FORM NB2).
RX MEDLINE-95014432; PubMed-7929319;
RA O'Neal K.D., Yu-Lee L.Y.;
RT "Differential signal transduction of the short, Nb2, and long
RT prolactin receptors. Activation of interferon regulatory factor-1 and
RT cell proliferation.";
RL J. Biol. Chem. 269:26076-26082(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING OF THE PRLR GENE.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
EMBL; M57668; AAA41938.1; -
DR EMBL; M34083; AAA79273.1; -
DR EMBL; L48060; AAA79274.1; -
DR EMBL; U34730; AAA92053.1; -
DR EMBL; M19304; AAA41937.1; -
DR EMBL; M74152; AAA41946.1; -
DR EMBL; U07567; AAA61784.1; -
DR PIR; A29884; A29884.
DR HSSP; P16471; LBP3.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 610 PROLACTIN RECEPTOR.
FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 230 253 BY SIMILARITY.
FT DOMAIN 254 610 CYTOPLASMIC (BY SIMILARITY).
FT DOMAIN 20 117 FIBRONECTIN TYPE-III.
FT DOMAIN 119 222 FIBRONECTIN TYPE-III.
FT DISULFID 31 41 BY SIMILARITY.
FT DISULFID 70 81 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .).

```

FT	DOMAIN	123	227	FIBRONECTIN TYPE-III.
FT	DISULFID	36	46	BY SIMILARITY.
FT	DISULFID	75	86	BY SIMILARITY.
FT	CARBOHYD	59	59	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	233	233	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	581 AA; 65159 MW; 975E47CB63CF28EC CRC64;		

Query Match 8.8%; Score 201; DB 1; Length 581;
Best Local Similarity 26.3%; Pred. No. 7.9e-07;
Matches 60; Conservative 31; Mismatches 101; Indels 36; Gaps 9;

QY	112	PPARP-VVSCQAADYENFSCWSPSQISGLTPRYLTLSYRKKTIVLGADSQRRSPSTGWPWC	170
DB	27	PPGPKIIKCRSPGKETFTCWEPGSDGLPTNTLYHKE-----GETLIHEC	75
QY	171	PQDPLGCAARCVRVH---AEFWQYRINVTENVPLGGASTRLLDVSLQSLIRPPOPGQLRV	227
DB	76	PDYKTGPNPCYFSKSKHTSIWKIYIVITVNAINGVSSDPLXVDVYIYVEPEPANLTL	135
QY	228	ESVPGYPRG--LRASWTYP-----ASWPCQPHFLKFLQYRPAQHPANSTVEPAGLEE	279
DB	136	ELKHPEDRKPYLWKVFPPLTLDVKSQW-----FMQIYEIRLKPETAADWEIHPAAKQTQ	190
QY	280	V-ITDAVAGLPHAVRYSARDFLDAGTWSTWSPAWGTPPTCTTKEIP	326
DB	191	LKTFSLYPGKYLQVVRCKP--DHGYWSEWSPE-----SSIOIPNDPFP	231

RESULT 13
PRLR_RABIT
ID PRLR_RABIT STANDARD; PRT; 616 AA.
AC PL4787;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PRLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
OX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RC MEDLINE=89184578; PubMed=2928321;
RA Edery M., Jolicoeur C., Levi-Meyuets C., Dusanter-Fourt I.,
RA Petridou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;
RT "Identification and sequence analysis of a second form of prolactin
RT receptor by molecular cloning of complementary DNA from rabbit
RT mammary gland.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
RN [2]
RP 3D-STRUCTURE MODELING OF 30-228.
RX MEDLINE=97248733; PubMed=9094747;
RA Halaby D., Thoreau E., Djiane J., Mornon J.P.;
RT "Homology modeling of rabbit prolactin hormone complexed with its
RT receptor.";
RL Proteins 27:459-468(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PRLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).

```

229 SVPGYPRG-----LRASWYTPASWPCQPHLLKFRLOYRPAQHPANSTVEPAGLEE--VI 281
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 T-----KRSANIMYLWAKWSPLADASSNNHLYHYELRIKPEEKKEWETIS-VGVQTCKI 191
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 282 TDAVAGLPHAVRYSARDFLDAGTWSTWSPSAWGTPSTGTIPKELPAWGQLHTQPEVE-- 338
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 NRLNAGHRYVQV--RCTLDPGWSEWSESRHLLIFSGSQPPKPTIIKCRS-PEKETFT 248
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 339 -----PQVDSAPPRPSLQPHRLLDHRDSVEQV 367
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 249 CWKKPGLDGGHPTNYT-----LLYSKEGEEQV 275
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
PRLR_BOVIN STANDARD; PRT; 581 AA.
AC Q28172;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
OX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium.
RX MEDLINE=93246019; PubMed=1338725;
RA Scott P., Kessler M.A., Schuler L.A.;
RT "Molecular cloning of the bovine prolactin receptor and distribution
RT of prolactin and growth hormone receptor transcripts in fetal and
RT utero-placental tissues.";
RL Mol. Cell. Endocrinol. 89:47-58(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collabor
CC between the Swiss Institute of Bioinformatics and the EMBL outstat
CC the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no
CC modified and this statement is not removed. Usage by and for commo
CC entities requires a license agreement (See http://www.isb-sib.ch/anno
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L02549; AAA51417.1; -
CC HSSP; P14787; 1AN3.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_FL; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 258 POTENTIAL.
FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
FT DOMAIN 123 227 FIBRONECTIN TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 581 AA; 65153 MW; 7385C0D695EE139 CRC64;

```

```
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 1 23
FT DOMAIN 24 831
FT TRANSMEM 24 438
FT DOMAIN 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DOMAIN 36 46
FT DISULFID 75 86
FT DISULFID 59 91
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
FT CARBOHYD 335 335
FT SEQUENCE 831 AA; 94394 MW; 220916320F77FAC1 CRC64;

Query Match 10.4%; Score 236.5; DB 1; Length 831;
Best Local Similarity 29.6%; Pred. No. 4.2e-09;
Matches 80; Conservative 35; Mismatches 118; Indels 37; Gaps 13;

QY 113 PVPVSCQAADYENFSCWSPQISGLPTRYLTSYRKKTVLGADSRSPSTGPPWCP 171
DB 28 PGKPKIIRCSLEKETFCWKKPGSGDGLPTNTLYFSK-----DSEKI-----YEC 76

QY 172 Q-DPLGAARCVHG--AEFWSQYRINVTENVPLGASTRLDVSLSQILRPPDGLRVE 228
DB 77 DYRTSGPNSCYFNRYNTSWTTNTTATNEIGNSSDPQYVDVTSIVQPSVNLTL 136

QY 229 SVPGYPR--GLRASWTYPASWPCQPHELLKFLRYRPAQHPAWSTVEPAGLEE--VITDA 284
DB 137 T-QRYANIMYLWAKSPPLADASNLHYELRLKPEEKSEWTV-PVGVTQCKINRL 194

QY 285 VAGLPHAVRSARDFLDAGTWSPEAWGTSTGTIPKEIPAWGLHTQPEVE----- 338
DB 195 NAGMRVYVQV--RCMLDPCGESEWSSERRILISGGLSPPEKPTITKCRS-PEKETFTCW 251

QY 339 -QVDSAPPSPSLQPHRLDHRDSVEQV 367
DB 252 KFLDGGHPTNTY-----LLYSKEGEQV 275

RESULT 9
PRLR_COLLI STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cropsac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
receptor.";
```

SEQUENCE FROM N.A.
 Morris K.R., Strom A.D.G.;
 "Cloning and expression of biologically active porcine IL-6 receptor
 alpha chain."
 Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 123-186 FROM N.A.
 RC TISSUE=Liver;
 RA Klier J.J., Matteri R.L.;
 "Partial cDNA sequence of porcine interleukin 6 receptor."
 Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AF147881; AAF73109.1; -;
 DR EMBL: AF015116; AAB70916.1; -;
 DR HSSP: PF16471; IBP3.
 DR InterPro: IPR000950; -;
 DR InterPro: IPR001777; -;
 DR InterPro: IPR002465; -;
 DR InterPro: IPR003006; -;
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; ig; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Signal.
 FT SIGNAL. 1 19 BY SIMILARITY.
 FT CHAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 366 386 POTENTIAL.
 FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 193 BY SIMILARITY.
 FT DISULFID 47 96 BY SIMILARITY.
 FT DISULFID 121 132 BY SIMILARITY.
 FT DISULFID 165 176 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 467 AA; 51066 MW; A2B0B884EF21C502 CRC64;
 Query Match 14.7%; Score 336; DB 1; Length 467;
 Best Local Similarity 28.2%; Pred. No. 3.3e-16;
 Matches 129; Conservative 55; Mismatches 205; Indels 68; Gaps 19;
 QY 12 LVAVATALVSASSPCP-QAAGPPG-----VOYQPGRSVKLCQPGVTAGD--PVSW 59
 Db 1 MLAVGCALLTALLAAPGMALPRCCSKLEVAQDVLTLSPGASVLTLCPGGPGDNATHW 60
 QY 60 FR----DGEPKLGGPDSGLGHELVLAQADSTDEGTYICOTLGLGALGTVTLQIGYPPAR 115

Db 61 VLNRQVTGSP---DGRPAGVGRRLLLKSVQLSDSGNYSCTQ-DGVPAGSVRLLVADAPPEE 116
 QY 116 PVVSC-QAADYENFSCWSPSQISGLPTRYLTYSRKKTVILGADSQRRSP-STGPMWPCPD 173
 Db 117 POLSCPRKSPLSNVGCEMRP-----RSPSPPTTRAVLLVRKFQNSPVEDFQPC-QY 167
 QY 174 PLGAAR--CVVHGAEFWSQYRI-NVTEVNPLGGASTRLLOVLSQSLIRPDPPQGLRVESV 230
 Db 168 SLEAQREFCOLAVPEGDSNFHVTLCVANSAGSSQSPOTFEGYGILODPDPVNVITVSAY 227
 QY 231 PGVPRGLASWTVPASWPCQPHFLKFLQVLRPAQHAWSTVEPAGLEE--VITDAVAGL 288
 Db 228 DRNPRWLSVTWQDPPSWNSY-FYRLQFLRLRAERSFTFTTWVWKELQHCIIHDWSGM 286
 QY 289 PHAVRSARDFLDAGTWSTWSPAWGTPTST---GTTPKEIPAWGQLHTQPEVEPQVDSP 344
 Db 287 RHVVQLRAQEEFGHGLWSEWSQEVGTGPWTERSSPAETELPLSTQATPTTNEDEDESSK 346
 QY 345 APPRPSLOPHRLDHRDSVEQVAVLASGLILSLGLVAGALGALGLRLRRGG-----K 399
 Db 347 ESANATSLP---VQDSASVPLPTFLVAGGSLAFGTL---LCIGIILRFKKTGLOALK 398
 QY 400 DGS-----PKPGFLASVIPVDRRPCAPN 422
 Db 399 EGKTNMHPYSLGQLVPERPKSTPVLVPLISPPVSPN 435
 RESULT 8
 ID PRLR_MELGA STANDARD; PRT; 831 AA.
 AC Q91094; Q91091; Q91092;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).
 GN PRLR.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97057891; PubMed=8902221;
 RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
 RT "Molecular cloning, tissue distribution, and expression of the
 RT prolactin receptor during various reproductive states in Meleagris
 RT gallopavo."
 RL Biol. Reprod. 55:1081-1090(1996).
 RN [2]
 RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 RC TISSUE=Ovary;
 RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: L76587; AAB01544.1; -;
 DR EMBL: U22947; AAA75038.1; -;
 DR EMBL: U22924; AAA75039.1; -;
 DR HSSP: PF16471; IBP3.
 DR InterPro: IPR000950; -;

CC BLOOD MONONUCLEAR CELLS AND WEAKLY FOUND IN URINE AND SERUM.
 CC -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -!- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE
 CC BY PROTEOLYSIS.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD126 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm"
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X12830; CAA31312.1; -;
 CC EMBL; X58298; CAA41231.1; -;
 CC EMBL; S72848; AAC60635.1; -;
 CC PIR; A41242; A41242;
 CC PIR; JU0080; JU0080;
 CC PIR; S14621; S14621;
 CC PIR; S17468; S17468;
 CC MIM; 147880; -;
 CC InterPro; IPR000950; -;
 CC InterPro; IPR001777; -;
 CC InterPro; IPR002465; -;
 CC InterPro; IPR003006; -;
 CC Pfam; PF00041; fn3; 1;
 CC Pfam; PF00047; ig; 1;
 CC PROSITE; PS01354; HEMATOPO_REC_L_F3; 1;
 CC Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 CC Alternative splicing; Signal.
 CC SIGNAL 1 19
 CC CHAIN 20 468 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 CC DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 366 386 POTENTIAL.
 CC DOMAIN 387 468 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 CC DISULFID 25 193
 CC DISULFID 47 96
 CC DISULFID 121 132
 CC DISULFID 165 176
 CC CARBOHYD 55 55
 CC CARBOHYD 93 93
 CC CARBOHYD 221 221
 CC VARSPLIC 356 365
 CC VARSPLIC 366 468 MISSING (IN SHORT ISOFORM).
 CC MUTAGEN 121 121 C->S: COMPLETE LOSS OF LIGAND-BINDING.
 CC MUTAGEN 122 122 E->A: NO CHANGE OF LIGAND-BINDING AND IL6
 CC SIGNALING.
 CC MUTAGEN 132 132 C->A: COMPLETE LOSS OF LIGAND-BINDING.
 CC MUTAGEN 134 134 W->L: COMPLETE LOSS OF LIGAND-BINDING.
 CC MUTAGEN 140 140 P->G: NO CHANGE OF LIGAND-BINDING AND IL6
 CC SIGNALING.
 CC MUTAGEN 153 153 E->L: NO CHANGE OF LIGAND-BINDING AND IL6
 CC SIGNALING.
 CC MUTAGEN 165 165 C->L: COMPLETE LOSS OF LIGAND-BINDING.
 CC MUTAGEN 174 174 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 CC SIGNALING.
 CC MUTAGEN 176 176 C->A: COMPLETE LOSS OF LIGAND-BINDING
 CC MUTAGEN 184 184 D->T: 30% DECREASE OF LIGAND-BINDING AND
 CC IL6 SIGNALING.
 CC MUTAGEN 190 190 V->G: 80% DECREASE OF LIGAND-BINDING AND
 CC NO IL6 SIGNALING.
 CC MUTAGEN 193 193 C->D: COMPLETE LOSS OF LIGAND-BINDING.
 CC MUTAGEN 211 211 C->A: NO CHANGE OF LIGAND-BINDING AND IL6
 CC SIGNALING.
 CC MUTAGEN 217 217 D->V: COMPLETE LOSS OF LIGAND-BINDING.

FT MUTAGEN 232 232 R->S: 30% DECREASE OF LIGAND-BINDING AND
 FT IL6 SIGNALING.
 FT MUTAGEN 233 233 W->O: 30% DECREASE OF LIGAND-BINDING AND
 FT INCREASE OF IL6 SIGNALING.
 FT MUTAGEN 254 254 E->A: 50% DECREASE OF LIGAND-BINDING AND
 FT IL6 SIGNALING.
 FT MUTAGEN 277 277 C->D: 30% INCREASE OF LIGAND-BINDING AND
 FT 100% INCREASE IN IL6 SIGNALING.
 FT MUTAGEN 278 278 V->N: 50% DECREASE OF LIGAND-BINDING AND
 FT 50% INCREASE IN IL6 SIGNALING.
 FT MUTAGEN 279 279 I->D: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 280 280 H->I: NO CHANGE OF LIGAND-BINDING AND NO
 FT IL6 SIGNALING.
 FT MUTAGEN 281 281 D->G: 70% DECREASE OF LIGAND-BINDING AND
 FT NO IL6 SIGNALING.
 FT MUTAGEN 285 285 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT NO IL6 SIGNALING.
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 SQ SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1B8B CRC64;
 Query Match 16.1%; Score 367.5; DB 1; Length 468;
 Best Local Similarity 28.4%; Pred. No. 2.3e-18;
 Matches 129; Conservative 56; Mismatches 198; Indels 71; Gaps 18;
 QY 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGD--PVS 58
 DB 2 LAVGCALLAALLAAPGAAL--APRCPAQAEVARGVLTSLPGDSVTLTCEGVPEPDNATVH 59
 QY 59 WFRDGEPKLQGPD-----SGLHELVLQAQADSTDEGTVCOTLDGALGGTVTLQGL 110
 DB 60 W-----VLRRPAAGSHPSRWAGMRLLRSVLHDSGNYSYRA-GRPAGTVHLLVD 111
 QY 111 YPARPVVSC-QAADYENFSCWSPQSGLPTRYLTYSRKTKVLGADSORBSPSTG-PW 168
 DB 112 VPPEEPQLSCFRKSPLSNVVCEWGRPTSLT-----KAVLLVRKFQNSPADFOE 163
 QY 169 PC-----PDPLGAARCVVHGAEFWSQYRLNVTENVPLGAGSTRLLDVSLQSLRDPDPOG 224
 DB 164 PCOYSQESQKFSQCLAVPEGDS--SFYIVSMCVASSVSGSKFSKTOTFOCGGILQPDPPAN 221
 QY 225 LRVESVPGYPRGLRASWTYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLEE--VIT 282
 DB 222 ITVTAVARNPRLSVTQWDPHSWN--SSFYRLRFLRYRAERSKTFETTMVKDLQHCVIH 280
 QY 283 DAVAGLPHAVRVSRDFLDAGCTWSTWSPFANGCTPTGTIPKEIPAWGOLHTOPEVPOVD 342
 DB 281 DAWSLRHVVQLRAQEEFQGEWSEWSPFANGCTPTGTIPKEIPAWGOLHTOPEVPOVD 328
 QY 343 SPAPRPSLQPHRLLDHRDSVEQVAV-----LASGLISFLGLVAGALAG----- 389
 DB 329 TPMQALTTNKDDNLL-FRDSANATSLPVQDSSVPLPTFL-VAGSLAFGLTLLCIAIVL 386
 QY 390 ----LW-LRLRGGKDGSPKGFSLASVIPVDRRP 418
 DB 387 RFKKTWKLKALKEGKTSMHPPYSGLQVLPVRPRP 420
 RESULT 7
 IL6A_PIG STANDARD; PRT; 467 AA.
 ID IL6A_PIG
 AC O18796;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 GN IL6R.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; M73238; AAA35707.1; -
DR EMBL; L38025; AAA91337.1; -
DR EMBL; L38023; AAA91337.1; JOINED.
DR EMBL; L38022; AAA91337.1; JOINED.
DR EMBL; L38024; AAA91337.1; JOINED.
DR PIR; A40854; UHHUCN.
DR HSSP; P40189; LBQU.
DR MIM; I18946; -
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR InterPro; IPR003006; -
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 342 CILIARY NEUTROPHIC FACTOR RECEPTOR
FT PROPEP 343 372 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 96 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 201 302 FIBRONECTIN TYPE-III.
FT DUF 46 89 POTENTIAL.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 342 342 GPI-ANCHOR (POTENTIAL).
SQ SEQUENCE 372 AA; 40633 MW; B2F3F73DE8F8750E CRC64;

Query Match 16.2%; Score 369.5; DB 1; Length 372;
Best Local Similarity 30.0%; Pred. No. 1.3e-18;
Matches 122; Conservative 47; Mismatches 168; Indels 69; Gaps 16;
QY 12 LVAVATALVSASSPCQAGPPGVQVQPGQSRVSKLCCPGVTAGDPVSWFRDGPCKLLQGP 71
DB 12 VLAATAAVVYQHRSPQE--APHVQYERLGSVDVTLPCGTANMDAAVTRVNGTD---LAP 66
QY 72 DSGLGHVLVLAQADSDTEGYICQTLDG-ALGGTVTLQLCYPPARVVSQAAADY-ENFS 129
DB 67 DLLNGSQLVHLGLEHSGHLYACFHRDSWHLRHQVLLHVLGPPREPVLSCRNTYPKGFY 126
QY 130 CTWSPSQISGLPT-RYLTYSVRKTVLGCADSQRRSPSTGWPCCPQDPLGAARCVVHGAEEF 188
DB 127 CSWH-----LPTPTVPTFNTVTLHGSK-----INVCEKDPALKNRCHIRYMHLF 172
QY 189 S--OYRINTEVNPGLGASTRLDLVLSQSLRDPDQGLRVESVPGYRGLRASWTYPAS 246
DB 173 STIKYKVSISVSNALGNHNAITFOEF-TIVKDPDPENVARVPSPNRRLEVTWQTPT 231
QY 247 WPCQPHFLKFRLOYPAQHPANSTVEPA-GLEEVITDAVAGLPHAVRVSAFDFLAGTW 305
DB 232 WPDPSFPLKFLRYRPLRLDQHQHVELSDGTAHTITDAYAGREYTIQVAAKD-NEIGTW 290
QY 306 STWSPAWGTPTGTTPKEIPKIPANGQLHTQPEVPEQVDSPPRPSLQHPRLDLDRDSVE 365
DB 291 SDWSVAHAATPTEE-PRHLLTTEAQ--AAETTTSTTSSSLAPP-----PTTKICD----- 336
QY 366 QVAVLASGLTSLGLVAGALALGLWLRRRGGKDGSPKPGFLASV 411
DB 337 -----PGEL-----GSGGSPSAPFLVSV 354

RESULT 6
IL6A_HUMAN
ID IL6A_HUMAN STANDARD; PRT; 468 AA.

AC P08887; Q16202;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1)
DE (CD126 ANTIGEN).
GN IL6R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=88305347; PubMed=3136546;
RA Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA Taniguchi T., Hirano T., Kishimoto T.;
RT "Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2)
RT receptor.";
RL Science 241:825-828(1988).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RA Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA Taniguchi T., Hirano T., Kishimoto T.;
RT "Molecular structure of interleukin 6 receptor.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).
RN [3]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=91336983; PubMed=1872801;
RA Schootlink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,
RA Kishimoto T., Heinrich P.C., Rose-John S.;
RT "Structural and functional studies on the human hepatic interleukin-6
RT receptor. Molecular cloning and overexpression in HepG2 cells.";
RL Biochem. J. 277:659-664(1991).
RN [4]
RP SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).
RX MEDLINE=94333499; PubMed=8056053;
RA Horiuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,
RA Matsumoto A., Yamamoto M., Yamamoto N.;
RT "Soluble interleukin-6 receptors released from T cell or
RT granulocyte/macrophage cell lines and human peripheral blood
RT mononuclear cells are generated through an alternative splicing
RT mechanism.";
RL Eur. J. Immunol. 24:1945-1948(1994).
RN [5]
RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=99167486; PubMed=10066782;
RA Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,
RA Moritz R.L., Simpson R.J.;
RT "Disulfide bond structure and N-glycosylation sites of the
RT extracellular domain of the human interleukin-6 receptor.";
RL J. Biol. Chem. 274:7207-7215(1999).
RN [6]
RP MUTAGENESIS.
RX MEDLINE=93223711; PubMed=8467812;
RA Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibl M.,
RA Taga T., Kishimoto T.;
RT "Structure-function analysis of human IL-6 receptor: dissociation of
RT amino acid residues required for IL-6-binding and for IL-6 signal
RT transduction through gp130.";
RL EMBO J. 12:1705-1712(1993).
CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC REACTIONS AND HEMATOPOIESIS.
CC -!- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6
CC RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.
CC -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
CC SECRETED (SHORT FORM).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL

DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR (CNTFR ALPHA)
DE (GROWTH PROMOTING ACTIVITY RECEPTOR ALPHA) (GPA RECEPTOR ALPHA) (GPAR
DE ALPHA).
GN CNTFR.
OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96064819; PubMed=7595532;
RA Ip F.C.F., Fu A.K.Y., Tsui K.W.K., Ip N.Y.;
RT "Cloning of the alpha component of the chick ciliary neurotrophic
RT factor receptor: developmental expression and down-regulation in
RT denervated skeletal muscle."
RL J. Neurochem. 65:2393-2400(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95401882; PubMed=7671828;
RA Heller S., Finn T.P., Huber J., Nishi R., Geissen M., Pueschel A.W.,
RA Rohrer H.;
RT "Analysis of function and expression of the chick GPA receptor (GPAR
RT alpha) suggests multiple roles in neuronal development."
RL Development 121:2681-2693(1995).
CC -!- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE
CC RECEPTOR SPECIFICITY.
CC -!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN NERVOUS SYSTEM. ALSO FOUND
CC IN SKELETAL MUSCLE.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U29245; AAA87838.1; -;
DR EMBL; Z48168; CAA88184.1; -;
DR HSSP; P16471; IBP3.
DR InterPro; IPR000950; -;
DR InterPro; IPR001777; -;
DR InterPro; IPR002465; -;
DR InterPro; IPR003006; -;
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR PROSITE; PS01354; HDMATOPO_REC_L_F3; 1.
KW Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT CHAIN 20 334
FT
FT CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT ALPHA.
FT
FT PROPEP 335 362
FT DOMAIN 37 94
FT DOMAIN 199 300
FT
FT DISULFID 44 87
FT CARBOHYD 58 58
FT CARBOHYD 68 68
FT CARBOHYD 140 140
FT CARBOHYD 188 188
FT LIPID 334 334
FT CONFLICT 337 337
FT SEQUENCE 362 AA; 40307 MW; 5A90217EB48419F7 CRC64;

Query Match

16.2%; Score 369.5; DB 1; Length 362;

Best Local Similarity 30.5%; Pred. No. 1.2e-18;
Matches 120; Conservative 51; Mismatches 165; Indels 57; Gaps 17;
Qy 2 SSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYGGPGRSVKLCPCPGVTAGDPVSMFR 61
Db 7 SACCVVLAADVAVVVVTAQRHSQODS-----HIQYERGVADVTMKCGSMDWDAAVTWA 57
Qy 62 DGEPKLLQGPDSGL-GHELVLAQADSTDEGTYICOTLDGA---LGGTVTLQLGYPPARPV 117
Db 58 NG----TDIDSHLNGSYLLKNVDLTQSGYSC--YEGSSWHLKYQTYLRVGVPPKEPV 111
Qy 118 VSCQAADY-ENFSCWTS-PSQISGLPTRYLYTSYRKKTVLGADSQRRSPSTGFWPCQDPL 175
Db 112 LMCRSNNYPKGYCSWHLPS-----PTVIPSFNISVTHG-----TREMWEKIDIF 157
Qy 176 GAARCVVHGAEFWS--OYRINVTENVPLGGASTRLDVSLOSILRPPDPQGLRVESVPGY 233
Db 158 PKNRCHIRYLQFLSTVKYKVTTLVTNALGKNSTTLTFDEF-AIVKADPPESVVAKPVPNN 216
Qy 234 PRGLRASWTYPASWPCQPHFLKFLRLOYRPAQHPAWSTVEPA-GLEEVITDAVAGLPHAV 292
Db 217 PRLVSVHQNQSSWPDPSFPLKFLRYRPLILDQWQHVELSDGTSHTITDAYAGKEYII 276
Qy 293 RVSARDFLDAGTWTSPEAWGTSTGTIPKEIPAWGQLTHQPEVEPOVDSPPAPRPSLQ 352
Db 277 QVAARK-NDIGTWSDSVAVHATPWTEE-PKHLTT--EVQITETTTSTSTSSFMPP----- 327
Qy 353 PHPRLLDHRDSVEQVA-----VLASLGIL 376
Db 328 PTTKICDKGAGVGSAGAVACWTAGLVLAAYGVL 360
RESULT 5
ID CNTR_HUMAN STANDARD; PRT; 372 AA.
AC P26992;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR (CNTFR ALPHA).
GN CNTFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91289158; PubMed=1648265;
RA Davis S., Aldrich T.H., Valenzuela D.M., Wong V., Furth M.E.,
RA Squinto S.P., Yancopoulos G.D.;
RT "The receptor for ciliary neurotrophic factor."
RL Science 253:59-63(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95293367; PubMed=7774913;
RA Valenzuela D.M., Rojas E., le Beau M.M., Espinosa R.,
RA Brannan C.I., McClain J., Masiakowski P., Ip N.Y., Copeland N.G.,
RA Jenkins N.A., Yancopoulos G.D.;
RT "Genomic organization and chromosomal localization of the human and
RT mouse genes encoding the alpha receptor component for ciliary
RT neurotrophic factor."
RL Genomics 25:157-163(1995).
CC -!- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE
CC RECEPTOR SPECIFICITY.
CC -!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM AND SKELETAL MUSCLE.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

QY 1 MSSSCGLSRVLVAVATALVSASSPCQAWPGPVGYGQGRSVKLCCEGVTAGD--PVS 58
 Db 2 LAVGCTLLVALLAAPVALVLS--CRALEAVANGTSLPGATVTLTCGKEAAGNATH 59
 QY 59 WFRDGEPLKLOGPD-SGLGHELVLAQADSTDEGTTCYICQTLGDLGALGCTVTLQGYPPARPV 117
 Db 60 WYVSGS-----QSEWTTTNTLRAVQVNDTGHYLC-FLDDHLVGTVPFLLDVDPPEPK 114
 QY 118 VSC-QAADYENFSCWSPQISGLPTRYLSYRKTKVLGADSORRSPSTGPPWPCP-QDPL 175
 Db 115 LSCFRKNPLNFAECWHPSTPS-PTTKAVFAKKI-----NTNKGSDFOVPCQYSQQL 168
 QY 176 GAARCVVHGAEFWSQVRI-NVTEVNPGLGASTRLLDVLSQSI--LRPDPQGLRVESVPG 232
 Db 169 KSPCEVEILEGDKVYHIVSLCVANSVGRSSH--NVVFQSLKMWQDPDPPANLVSAIPG 226
 QY 233 YPGLRASWTYPASWPCQPHFLKFLRLOYRPAQHAWPS-----IVPEAGLEE---VITDAVA 286
 Db 227 XPRWLKVSQWODPESWD-PSYLLQFELRYR-----PWSKXFTVMPLOVAHQCVIHDALR 281
 QY 287 GLPHAVRVSAARDPLDAGTWSTWSPSANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPAP 346
 Db 282 GYKHVVQVRGKEEFDIGQSKSPVETGTP-----W---LAEPRTTTPAGIPGNP 327
 QY 347 PRPSLOPHRLDHRD-----SVEQVAVLA-----SLGILSFLGLVAGALAGLW----- 391
 Db 328 TVQSVEDYD---NHEDQYSSTSEATSVLAPVQSGSPPLPTFL-VAGSGSLAFGLLLCVFI 383
 QY 392 -LRLRGGKD-----GSPKPGFLASVIVDRRPGAPN 422
 Db 384 ILRLKKKKWSQAEKESKTTSPPPYPLGLPKPTFL--LVPLLTSPSGSHN 429

RESULT 3
 CNTR_RAT CNTR_RAT STANDARD; PRT; 372 AA.

AC Q08406;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR (CNTRF ALPHA).
 GN CNTRF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93152175; PubMed=8381290;
 RA Ip N.Y., McClain J., Barrezaeta N.X., Aldrich T.H., Pan L., Li Y.,
 RA Wiegand S.J., Friedman B., Davis S., Vancopoulos G.D.;
 RT "The alpha component of the CNTRF receptor is required for signaling
 RT and defines potential CNTRF targets in the adult and during
 RT development.";
 RL Neuron 10:89-102(1993).
 RN [2]
 RP SEQUENCE OF 185-277 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=93211934; PubMed=8460125;
 RA Clatterbuck R.E., Price D.L., Koliatsos V.E.;
 RT "Ciliary neurotrophic factor prevents retrograde neuronal death in
 RT the adult central nervous system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2222-2226(1993).
 CC -!- FUNCTION: BINDS TO CNTRF (GPA). THE ALPHA CHAIN PROVIDES THE
 CC RECEPTOR SPECIFICITY.
 CC -!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GPI30.
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S54212; AAB25290.1; -
 DR EMBL: S57711; AAB25918.1; -
 DR PIR: A47387; A47387.
 DR InterPro: IPR000950; -
 DR InterPro: IPR001777; -
 DR InterPro: IPR002465; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00041; f03; 1.
 DR Pfam: PF00047; f03; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 KW Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 342
 FT CILIARY NEUROTROPHIC FACTOR RECEPTOR
 FT ALPHA.
 FT PROPEP 343 372
 FT DOMAIN 39 96
 FT DOMAIN 201 302
 FT DISULFID 46 89.
 FT CARBOHYD 60 60
 FT CARBOHYD 70 70
 FT CARBOHYD 142 142
 FT CARBOHYD 190 190
 FT CARBOHYD 261 261
 FT LIPID 342 342
 FT CONFLICT 261 261
 FT N -> D (IN REF. 2).
 SQ SEQUENCE 372 AA; 40822 MW; 3B87EE63923FB149 CRC64;

Query Match 16.4%; Score 374.5; DB 1; Length 372;
 Best Local Similarity 31.5%; Pred. No. 5.8e-19;
 Matches 112; Conservative 49; Mismatches 165; Indels 29; Gaps 13;

QY 1 MSSSCGLSRVLVAVATALVSASSPCQAWPGPVGYGQGRSVKLCCEGVTAGDPSVWF 60
 Db 1 MAASVPWACCAALAAAAAAYTKHSPQE--APHVQYERLGTDTVLPCCGTASWDAAVTWR 58
 QY 61 RQCEPKLLQGGPSGLGHELVLAQADSTDEGTTCYICQTLGDLG-ALGCTVTLQGYPPARPVVS 119
 Db 59 VNGTD---LAPDLLNGSLILSLGSLGSLYACFHRDSHLRHQVLLHVLGLPPREPVL 115
 QY 120 CQAADY-ENFSCWSPQISGLPTRYLSYRKTKVLGADSORRSPSTGPPWPCQDPLGAA 178
 Db 116 CRSNTYKGYFCWSHLS---APT-YIPNTFNTVTLGSKN-----MVCEKDPALKN 162
 QY 179 RCVVHGAEFWS--QYRINTVNPGLGASTRLLDVLSQSI--LRPDPQGLRVESVPGYPRG 236
 Db 163 RCHIRYMHLEFTIKYKVSISVSNAL-GHNTTATTFDEFTIKVDPDPENVVAVRVPSPNRR 221
 QY 237 LRASWTYPASWPCQPHFLKFLRLOYRPAQHAWPSVPEA-GLEEVITDAVAGLPHAVRV 295
 Db 222 LEVWTQTPSTWDPESFPLKFFLYRPLLDQWQHVSLSNGTAHTITDAYAGKEYLIQVA 281
 QY 296 ARDLDAGTWSTWSPSANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPAPPRPS 350
 Db 282 AND-NEIGTWSWDSVAHAATPWTEE-PRHLTTEAQ---APETTTTSSSLAPPPT 331

RESULT 4
 CNTR_CHICK
 ID CNTR_CHICK STANDARD; PRT; 362 AA.
 AC P51541;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2001, 17:34:32 ; Search time 15.19 Seconds
(without alignments)
953.922 Million cell updates/sec

Title: US-09-532-263-5
Perfect score: 2282
Sequence: 1 MSSSCSGLSRVLVAVATALV.....KPGFLASVIPVDRRPGAPNL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	402	17.6	460	1	IL6A_MOUSE	P22272 mus musculus
2	398	17.4	462	1	IL6A_RAT	P22273 rattus norv
3	374.5	16.4	372	1	CNTR_RAT	Q08406 rattus norv
4	369.5	16.2	362	1	CNTR_CHICK	P51641 gallus gall
5	369.5	16.2	372	1	CNTR_HUMAN	P26992 homo sapien
6	367.5	16.1	468	1	IL6A_HUMAN	P08887 homo sapien
7	336	14.7	467	1	IL6A_PIG	O18796 sus scrofa
8	236.5	10.4	831	1	PRIR_MELGA	Q91094 meleagris g
9	222.5	9.8	830	1	PRIR_COLLI	Q90374 columba liv
10	216.5	9.5	831	1	PRIR_CHICK	Q04594 gallus gall
11	207	9.1	581	1	PRIR_BOVIN	Q28172 bos taurus
12	201	8.8	581	1	PRIR_CEREL	Q28235 cervus elap
13	195.5	8.6	616	1	PRIR_RABIT	P14787 oryctolagus
14	191.5	8.4	610	1	PRIR_RAT	P05710 rattus norv
15	189.5	8.3	622	1	PRIR_HUMAN	P16471 homo sapien
16	183.5	8.0	327	1	IL2B_CAPHI	O18989 capra hircu
17	183.5	8.0	1266	1	NGCA_CHICK	Q03696 gallus gall
18	181.5	8.0	327	1	IL2B_MARMO	Q61729 marmota mon
19	180	7.9	630	1	PRIR_ORENI	Q91513 oreochromis
20	179.5	7.9	327	1	IL2B_BOVIN	P46282 bos taurus
21	175.5	7.7	327	1	IL2B_CEREL	Q28234 cervus elap
22	175.5	7.7	608	1	PRIR_MOUSE	Q08501 mus musculus
23	171	7.5	324	1	IL2B_PIG	Q28938 sus scrofa
24	167	7.3	329	1	IL2B_FELCA	Q02744 felis silve
25	165	7.2	761	1	NCAL_HUMAN	P13592 homo sapien
26	163.5	7.2	327	1	IL2B_SHEEP	O02815 ovis aries
27	163	7.1	328	1	IL2B_MACMU	P48095 macaca mula
28	160	7.0	328	1	IL2B_HUMAN	P29460 homo sapien
29	155.5	6.8	918	1	IL6B_HUMAN	P40189 homo sapien
30	154.5	6.8	329	1	IL2B_HORSE	Q9X8Q5 equus cabal
31	149.5	6.6	836	1	GCSR_HUMAN	Q99062 homo sapien
32	148	6.5	853	1	NCAL_BOVIN	P18336 bos taurus
33	146	6.4	917	1	IL6B_MOUSE	Q00560 mus musculus

34	145	6.4	328	1	IL2B_CERTO	P45658 cercocebus
35	145	6.4	858	1	NCAL_RAT	P13596 rattus norv
36	144	6.3	329	1	IL2B_CANFA	Q28268 canis famil
37	144	6.3	848	1	NCAL_HUMAN	P13591 homo sapien
38	141	6.2	1162	1	LEPR_MOUSE	P48356 mus musculu
39	140	6.1	1897	1	PTPE_HUMAN	P10586 homo sapien
40	138.5	6.1	335	1	IL2B_MOUSE	P43432 mus musculu
41	138	6.0	890	1	TYO3_HUMAN	Q08418 homo sapien
42	138	6.0	1092	1	LIFR_MOUSE	P42703 mus musculu
43	134.5	5.9	297	1	GHRH_MOUSE	P16590 mus musculu
44	134.5	5.9	650	1	GHRH_MOUSE	P16882 mus musculu
45	133.5	5.9	638	1	GHR_RAT	P16310 rattus norv

ALIGNMENTS

RESULT 1

ID IL6A_MOUSE STANDARD; PRT: 460 AA.
AC P22272;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
GN IL6RA OR IL6R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Spleen;
RX MEDLINE=90278354; PubMed=2112585;
RA Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA Kishimoto T.;
RT "Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytogenesis.";
RL J. Exp. Med. 171:2001-2009(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H; TISSUE=Liver;
RA Fiorillo M.T., Ciliberto G., Dente L.;
RA Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
RL CC
CC 1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC REACTIONS AND HEMATOPOIESIS.
CC 1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
CC SIMILARITY).
CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC 1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC 1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC 1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC 1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; X51975; CAA36237.1; .
EMBL; X53802; CAA37810.1; .
PIR; JLO144; JLO144.
PIR; JLO145; JLO145.
PIR; S14543; S14543.
HSSP; P16471; 1BP3.

THIS PAGE BLANK (USPTO)

F:235-258/Domain: transmembrane #status predicted <TM>

F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.6%; Score 195.5; DB 2; Length 616;
Best Local Similarity 27.3%; Pred. No. 1.3e-05;
Matches 65; Conservative 28; Mismatches 98; Indels 47; Gaps 13;

QY 112 PPARP-VVSCQAADYENFSCWSPSOISGLPTRYLTYSRKKTVLGADSORRSPSTGPWPC 170

DB 27 PPGKPEIHKCRSPDKETFTCWNPNGTDGLPTNYSLTYSKEGKTT-----GETITHEC 75

QY 171 PQDPLGAARCVVHGAEF---AEFWQYRINVTENVPLGG--ASTRLLDVLSQSLRPDPPOGL 225

DB 76 PDKTGGPNSCFYSKHTSIWIIYIIVNATNQMGSSVSDPRYVDVY--IVEPDPVNL 133

QY 226 RVESVPGYPRG--LRASWTYP-----ASWPCQPHFLKFRQYRPAQHPANSTVEPAGL 277

DB 134 TLEVKHPEDRKPYLWVKWLPPTLVDRSGW-----LTLOYEIRLKEKAHEWET-HFAGQ 187

QY 278 EE--VITDAVAGLPHAVRVSARDFLDAGTWSTWSPWAMCTPSTGTIP-----KEIPAW 328

DB 188 QTOFKILSLYPGQKYLQVRCRP--DHGFWSVMSPE-----SSIQIPNDFTMKDITVW 238

RESULT 14

A29884

prolactin receptor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000

C:Accession: A29884

Cell 53, 69-77, 1988

A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho

A:Reference number: A29884; MUID:88165059

A:Accession: A29884

A:Molecule type: mRNA

A:Residues: 1-310 <BOU>

A:Cross-references: GB:M19304; NID:g206364; PIDN:AAA41937.1; PID:g206365

C:Superfamily: cytokine receptor homology

C:Keywords: transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-310/Product: prolactin receptor #status predicted <MAT>

F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.4%; Score 191.5; DB 2; Length 310;
Best Local Similarity 24.8%; Pred. No. 1.1e-05;
Matches 54; Conservative 34; Mismatches 91; Indels 39; Gaps 10;

QY 112 PPARPVW-SCQAADYENFSCWSPSOISGLPTRYLTYSRK---KTVLGADSORRSPSTGP 167

DB 22 PPGKPEIHKCRSPDKETFTCWNPNGTDGLPTNYSLTYSKEGKTT----- 67

QY 168 WPCPDPLGAARCVVHGAEF---WSQYRINVTENVPLGGASTRLLDVLSQSLRPDPPOG 224

DB 68 YECPDYKTSKPNPSCFSGKQYTSWIKYIITVNATNQMGSSSDPLVVDVYIIVEPEPPRN 127

QY 225 --LRVESVPGYPRGLRASWTYP-----ASWPCQPHFLKFRQYRPAQHPANSTVEPAG 276

DB 128 LTVKQLKDKKTYLWVKWSPPTITDVKTWG-----FTMEYEIRLKEPEAEWE-IHFTG 181

QY 277 --LEEVIITDAVAGLPHAVRVSARDFLDAGTWSTWSPA 312

DB 182 HOTQFKVFDLYPGQKYLQVTRCKP--DHGYWSRWSQES 217

RESULT 15

A41070

prolactin receptor Nb2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 28-Jul-2000

C:Accession: A41070; I55417

R:Ali. S.; Pellegrini, I.; Kelly, P.A.

J. Biol. Chem. 266, 20110-20117, 1991

A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prol

A:Reference number: A41070; MUID:92041834

A:Accession: A41070

A:Molecule type: mRNA

A:Residues: 1-412 <ALI>

A:Cross-references: GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390

R:O'Neal, K.D.; Yu-Lee, L.Y.

J. Biol. Chem. 269, 26076-26082, 1994

A:Title: Differential signal transduction of the short, Nb2, and long prolactin recep

A:Reference number: I55417; MUID:95014432

A:Accession: I55417

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-412 <RES>

A:Cross-references: EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PID:g641964

A:Experimental source: Nb2-11C cell line

C:Superfamily: cytokine receptor homology

C:Keywords: transmembrane protein

F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.4%; Score 191.5; DB 2; Length 412;
Best Local Similarity 24.8%; Pred. No. 1.5e-05;
Matches 54; Conservative 34; Mismatches 91; Indels 39; Gaps 10;

QY 112 PPARPVW-SCQAADYENFSCWSPSOISGLPTRYLTYSRK---KTVLGADSORRSPSTGP 167

DB 22 PPGKPEIHKCRSPDKETFTCWNPNGTDGLPTNYSLTYSKEGKTT----- 67

QY 168 WPCPDPLGAARCVVHGAEF---WSQYRINVTENVPLGGASTRLLDVLSQSLRPDPPOG 224

DB 68 YECPDYKTSKPNPSCFSGKQYTSWIKYIITVNATNQMGSSSDPLVVDVYIIVEPEPPRN 127

QY 225 --LRVESVPGYPRGLRASWTYP-----ASWPCQPHFLKFRQYRPAQHPANSTVEPAG 276

DB 128 LTVKQLKDKKTYLWVKWSPPTITDVKTWG-----FTMEYEIRLKEPEAEWE-IHFTG 181

QY 277 --LEEVIITDAVAGLPHAVRVSARDFLDAGTWSTWSPA 312

DB 182 HOTQFKVFDLYPGQKYLQVTRCKP--DHGYWSRWSQES 217

Search completed: August 24, 2001, 17:33:27

Job time: 145 sec

F:23-818/Product: prolactin receptor 2#status pl
F:36-221/Domain: cytokine receptor homology <CRS>

A:Reference number: A40854; MUID:91289158

A:Accession: A40854

A:Molecule type: mRNA

A:Residues: 1-372 <DAV>

A:Cross-references: GB:M73238

R:Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.L.; McClain, Genomics 25, 157-163, 1995

A:Title: Genomic organization and chromosomal localization of the human and mouse genes

A:Reference number: A56526; MUID:95293367

A:Accession: A56526

A:Molecule type: DNA

A:Residues: 1-346, S', 348-372 <VAL>

A:Cross-references: GB:L38025; NID:9608654; PIDN:AAA91337.1; PID:9608656

C:Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylinositol

C:Genetics:

A:Gene: GDB:CNTRF

A:Cross-references: GDB:134652; OMIM:118946

A:Map position: 9p13-9p13

C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunoglobulin-like receptor; growth factor receptor; membrane protein; phosphatidylinositol

F:1-372/Domain: signal sequence #status predicted <SIG>

F:21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>

F:39-91/Domain: immunoglobulin homology <IMM>

F:116-296/Domain: cytokine receptor homology <CRS>

F:46-89/bisulfide bonds: #status predicted

F:60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.1%; Score 366.5; DB 1; Length 372;
Best Local Similarity 30.0%; Pred. No. 4.1e-17;
Matches 122; Conservative 47; Mismatches 168; Indels 69; Gaps 16;

QY 12 LVAVATALVSASSPCQAWPGVQVQPGSRVSKLCCPGVTAGDPVSVFRDGPCKLQGP 71

DB 12 VLAARAAVYAQRHSQEE--APHVQVERLGSDVTLPCGTANWDAATVWRVNGTD---LAP 66

QY 72 DSGLGHVLAQADSTDEGTYICQTLDG-ALGCTVTQLQGYPPARVWSCAAADY-ENFS 129

DB 67 DLLNGSQLVHLGLHGLSHGLYACFRDSDHLRHQVLLHVLGPPREPVLSCRSNTYPKGFY 126

QY 130 CTWSPSQISGLPT-RVLTYSRKTKTVLGADSORSPSTGFWPCQDPDLGAAACVHVGAEFW 188

DB 127 CSWH-----LPTPTPIPTNFVNTLVHSGK-----IMVCEKDPALKNRCHIRYMHLF 172

QY 189 S--QYRINVTENPLGASATRLDLVLSQISLRDPDPOGLRVESVGPYRGLRASWTYPAS 246

DB 173 STIKYKVSIVSNALGHNAITAIFDEF-FIVKDPDENNVAVRVPNSRPRLEVTVWOTPST 231

QY 247 WPCQPHFLKFRLOYRPAQHPASTVEPA-GLEEVITDAVAGLPHAVRVASARDFLDAGTW 305

DB 232 WPDPEFPLKFFLYRPLLDQHQHVELSDGTAHTITDAYAGREYITQVAAKD-NEIGTW 290

QY 306 STWSPKAWGTPGTGTPKEIPANGQLHOTOPEVQVDSAPPRLSLOPHRLLDHRDSVE 365

DB 291 SDWSVAHAHATPWTEE-PRUTTEAQ--AAETTTSTTSSLAPP-----PTTKICD----- 336

QY 366 QVAVLASGLTSLGLVAGALALGLWLRRLRGCKGDSRKPGLASV 411

DB 337 -----PGEL-----GSGGGPCAPFLVSV 354

RESULT 9

A37986

Interleukin-6 receptor precursor - rat

N:Alternate names: IL-6 receptor

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #Text_change 22-Jun-1999

A:Accession: A37986

R:Baumann, M.; Baumann, H.; Fey, G.H.

J. Biol. Chem. 265, 19853-19862, 1990

A:Title: Molecular cloning, characterization and functional expression of the rat liver

A:Reference number: A37986; MUID:91060602

A:Accession: A37986

A:Molecule type: mRNA

A:Residues: 1-462 <BAU>

A:Cross-references: GB:M58587; GB:J05668; NID:9204921; PIDN:AAA41431.1; PID:9204922

C:Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is

C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immu

C:Keywords: acute phase; cytokine receptor; transmembrane protein

F:1-13/Domain: signal sequence #status predicted <SIG>

F:20-462/Product: interleukin-6 receptor #status predicted <MAT>

F:40-94/Domain: extracellular #status predicted <EXT>

F:117-306/Domain: immunoglobulin homology <IMM>

F:363-385/Domain: cytokine receptor homology <CRS>

F:386-462/Domain: transmembrane #status predicted <TMW>

F:47-92/Disulfide bonds: #status predicted

Query Match 13.4%; Score 306; DB 1; Length 462;

Best Local Similarity 27.1%; Pred. No. 4.9e-13;

Matches 132; Conservative 51; Mismatches 180; Indels 124; Gaps 25;

QY 1 MSSSCSGLSRVLVAVATALVSASSPCQAWPGVQVQPGSRVSKLCCPGVTAGD--PVS 58

DB 2 LAVGCTLLVALLAAPVALVLGS--CRALEVANGTVTSLECATVTLICPKKEAGNATHI 59

QY 59 WFRDGPCKLQGPD-SGLGHVLAQADSTDEGTYICQTLDGALGCTVTQLQGYPPARV 117

DB 60 WYVSGS---QSREWTTTNTLVRAVQVNDTGHYLC-FLDDHLVGTVPVLLVDVPPPEPK 114

QY 118 VSC-QAADYENFSCWSPSQISGLPTRYLTYSRKTKTVLGADSORSPSTGFWPCP-QDPL 175

DB 115 LSCFRKNPLVNAFCEWHPSSTPS-PTTKAVMFAKKI-----NTTNGKSDQVPCQYSQOL 168

QY 176 GAARCVVHGAEFWSQYRI-NVTEVNPLGGASTRLLDVSQSI--LRPDPQGLRVESVPG 232

DB 169 KSPSCEVEILGDKVTHIVSLCVANSVSGSRSH--NVVFQSLKMWQDPPANLVWSAIPG 226

QY 233 -----YPRGLRASWTYPASWPCQPHFLKFRLOYRPAQHP 267

DB 227 SLVGSKSVGKTLSPGTQVTTCCNSSEFDTLYGQRTETV-WPLQ-----VAQHQ 273

QY 268 AMSTVEPAGLEEVITDAVAGLPHAVRVASARDFLDAGTWSVSPANGTPTGTIPIKEIPA 327

DB 274 C-----VIHDALRGVHVQVGRKEEDFDIGQWSKWSPEVTGTP----- 311

QY 328 WQQLHTQPEVQVDSAPPRLSLOPHRLLDHRD---SVEQVAVLA-----SLGILS 377

DB 312 W---LAEPRTTAPAGIPGNTOVSVEYD---NHEDQYGSSTEATSVLAPVQGSPIPLPT 365

QY 378 FLGLVAGALALGLW-----LRLRRGGKD-----GSPKPGFLASVPIVD 415

DB 366 FL-VAGSGLAFGLLLCVFIILRLKKWKSQAESKSTTSPPPYPLGLPKPTFL--LVPLL 422

QY 416 RRPQAPN 422

DB 423 TPGSGSHN 429

RESULT 10

I50455

prolactin receptor - pigeon

C:Species: Columba livia (domestic pigeon)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1995 #text_change 28-Jul-2000

A:Accession: I50455

R:Chen, X.; Horseman, N.D.

Endocrinology 135, 269-276, 1994

A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin recepto

A:Reference number: I50455; MUID:94283367

A:Accession: I50455

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-830 <CHE>

A:Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382

A:Molecule type: mRNA

A:Residues: 1-362 <HEL>
A:Cross-references: EMBL:Z48168; NID:G971417; PIDN:CAA88184.1; PID:G3063774
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin-6 receptor
C:Keywords: growth factor receptor
F:2-89/Domain: immunoglobulin homology <IMM>
F:114-294/Domain: cytokine receptor homology <CRS>

Query Match 16.1%; Score 368.5; DB 2; Length 362;
Best Local Similarity 30.5%; Pred. No. 2.9e-17;
Matches 120; Conservative 51; Mismatches 165; Indels 57; Gaps 17;

QY 2 SSSCSGLSRVLAVATALVSASSPCQAWGPGVQYQGRSVKLCPCGVTAGDPSWFR 61

Db 7 SACCVVLAADVAAVYVYQRRHQDS-----HIQYERVGADVTMKCGSMDMDAAVTWTA 57

QY 62 DCEPKLLQGPSGL-GHEVLAAQADSTDEGYICOTLQGA---LGGTVTLQGLQPPARPV 117

Db 58 NG-----TDIDSHLNGSYLILKNVDLTQSGQYSC--YEGSSWHLKYQYLRVGVPPKEPV 111

QY 118 VSCQAAAY-ENFSCFWS-PSQISGLPTRYLTSYRKTKVLGADSQRRSPSTGWPQDPL 175

Db 112 LMCRRNNPKGYCSWHLPS-----PTIIPNSFNISVING-----TRMWCEKDI 157

QY 176 GAARCVVHGAEPWS--QYRINVTENPLGGASTRLLDVLSQILRPPQGLRVESVPGY 233

Db 158 PKNRCHIRYQLFSTVYKVTLTNTALGKNSLTITDEF-AIVKPDPPESVVAKPVPNN 216

QY 234 PGLRASWTYPASWPCQPHFLKFRLOYRPAQHPAMSTVEPA-GLEEVITDVAAGLPAHV 292

Db 217 PRLEVSQNPSSPDPESEFLKFLRYRLPDLQWVHLSGDTGSHITDAYAGKEVII 276

QY 293 RVSARDELDAQWTSWSPGANGTPTGTIPKEIPAWGOLHTQPEVQVDSAPPSPSLQ 352

Db 277 QVAARD-NDIGTWSQWSAVVHATPTEB-PKHLTT--EVOITETSTSTSPMPP----- 327

QY 353 PHPRLLDHRDSVEQVA-----VLASGLIL 376

Db 328 PTTKICDKGVGVSGAVAVCTAGVLAAAYGVL 360

RESULT 7

A:1242
N:Contains: interleukin-6 receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change 21-Jul-2000
C:Accession: A41242; J00080; S17468; A61459; S14621
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.
Science 241, 825-828, 1988
A:Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.
A:Reference number: A41242; MUID:88305347
A:Accession: A41242
A:Molecule type: mRNA
A:Residues: 1-468 <Y>
A:Cross-references: GB:M20566; NID:G33845; PIDN:CAA31312.1; PID:G33846
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.
Proc. Jpn. Acad. 64, 209-211, 1988
A:Title: Molecular structure of interleukin 6 receptor.
A:Reference number: J00080
A:Accession: J00080
A:Molecule type: mRNA
A:Residues: 1-468 <Y>
R:Schölkopf, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich
Biochem. J. 277, 659-664, 1991
A:Title: Structural and functional studies on the human hepatic interleukin-6 receptor.
A:Reference number: S17468; MUID:91336983
A:Accession: S17468
A:Molecule type: mRNA
A:Residues: 1-468 <Y>
A:Cross-references: EMBL:X58298; NID:G32580; PIDN:CAA41231.1; PID:G32581
A:Experimental source: hepatoma cell line HepG2

R:Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.

J. Exp. Med. 170, 1409-1414, 1989

A:Title: Soluble cytokine receptors are present in normal human urine.

A:Reference number: A61459; MUID:90010793

A:Accession: A61459

A:Molecule type: protein

A:Residues: 20-49 <NOV>

C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, an

C:Comment: This growth factor receptor does not have a tyrosine kinase domain.

C:Genetics:

A:Gene: GDB:IL6R

A:Cross-references: GDB:127966; OMIM:147880

A:Map position: lq21-lq21

C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu

C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-468/Product: interleukin-6 receptor #status predicted <MAT>

F:20-363/Domain: extracellular #status predicted <EXT>

F:40-98/Domain: immunoglobulin homology <IMM>

F:121-309/Domain: cytokine receptor homology <CRS>

F:364-386/Domain: transmembrane #status predicted <TM>

F:387-468/Domain: intracellular #status predicted <INT>

F:47-96/Disulfide bonds: #status predicted

F:55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.1%; Score 367.5; DB 1; Length 468;

Best Local Similarity 28.4%; Pred. No. 4.5e-17;

Matches 129; Conservative 56; Mismatches 198; Indels 71; Gaps 18;

QY 1 MSSCSGLSRVLAVATALVSASSPCQAWGPGVQYQGRSVKLCPCGVTAGD--PVS 58

Db 2 LAVGCALLAALLAAPGAAL--APRRCPAQAVARGVLTSLPGDSVTLTCGPVEPEDNATVH 59

QY 59 WFDGEPEKLLQGD-----SGLGHELVLAQADSTDEGYICOTLQGLGCTVTLQGL 110

Db 60 W-----VLRKPAAGSHPSRWAGNRLLRLRSVQLHDSGNVSCYRA-GRPAGTVHLLVD 111

QY 111 YPPARPVYVSC-QAADYENFSCFWS-PSQISGLPTRYLTSYRKTKVLGADSQRRSPSTG-PW 168

Db 112 VPPEEPQLSCFKSPKPLSNVVCWGPSTPLTT-----KAVLLVRKFNQSPAEQOE 163

QY 169 PC-----PODPLGAARCVVHGAEPWSQYRINVTENPLGGASTRLLDVLSQILRPPDPOG 224

Db 164 PCQYQSQESQKFCQLAVPEGDS--SFYIVSMCVASSVSGSKFSTQTQFCGCGILOPPPAN 221

QY 225 LRVESVPGYPRCLRASWTYPASWPCQPHFLKFRLOYRPAQHPAMSTVEPAGLEE--VIT 282

Db 222 ITVTAVARNPRWLSVTWQDPHSWN--SSFYRLRFLRYRAERSKFTTWMVKDLQHHCVIH 280

QY 283 DAVAGLPHAVRSARDFLDAGTWSTWSPGANGTPTGTIPKEIPAWGOLHTQPEVQVDS 342

Db 281 DAWSLRHVVQLRAQEEFGQSEMSPEANGTPTWES-----RSSPAENEVS 328

QY 343 SPAPPRLSLQPHRLDHRDSVEQVAV----LASGLISFLGLVAGALAG----- 389

Db 329 TPMQALTINKDDNLL-ERDSANATSLPQDSSSVPLPTFL-VAGSLAFGLTLCIAIVL 386

QY 390 ---LW-LRLRGGKDGSPKPGCLASVLPVDRPP 418

Db 387 RPKKTKWLRALKEGKTSMHPPYSGLGVLPVRPRP 420

RESULT 8

UHHUCN

ciliary neurotrophic factor receptor alpha precursor - human

N:Alternate names: CNTR receptor

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C:Accession: A40854; A56526

R:Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.E.; Squinto, S.P.; Y

Science 253, 59-63, 1991

A:Title: The receptor for ciliary neurotrophic factor.

```
Db 229 RWLKVSQHPETWD-PSYLLQQLRYR-----PWSKEFTVLLPVAQYQCVIHDLRGV 283
QY 289 PHAVRVSARDFLDAGTWSTWSPAWCTPSTGTIPKEIPA---WGQLHTQPEVPEQVDSPA 345
Db 284 KHVVQVRGKEELDGLGQSEWSPVETGTPWIAE-PRITPAGILWNP--TQVSVE---DS-- 335
QY 346 PPRPSLQPHRLDHRD-----SVEQVAVILA-----SLGILSLGLVAGALGLW---- 391
Db 336 -----ANHEDQYESSTEATSVLAPVQESSMSLPTFL-VAGGSLAFGLLLCVF 382
QY 392 --LRLRGGKD-----GSPKPGFLASVIPVDRRGPAPN 422
Db 383 IILRLKQKWKSEAEKSTSPPPPPYSGLGPKLPTFLVPLLPHPSSGSDN 433

RESULT 4
JL0144
Interleukin-6 receptor precursor (clone lambda Pl) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0144
R:Sugita, T.; Totuska, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen
A:Reference number: JL0144; MUID:90278354
A:Accession: JL0144
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <SUG>
A:Cross-references: GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunog
C:Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-440/Product: interleukin-6 receptor #status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 17.4%; Score 396; DB 2; Length 440;
Best Local Similarity 32.1%; Pred. No. 5.6e-19;
Matches 134; Conservative 51; Mismatches 168; Indels 64; Gaps 21;

QY 1 MSSCSGLSRVLVAVATALVSASSPCQAWPGVQYQGPGRSVKLCPCGVTAGDPVVS-- 58
Db 2 LTGVTCLLVALLAAPAVALVLSG--CRALEVANGTVTSLSPGAIVTLICPKKEAAGNVTH 59
QY 59 WFRDGPKLQGPD-SGLGHELVLAQADSTDEGTTCQILDGALGCTVTLQLGYPARPV 117
Db 60 WYVSGS---QNRWTTTNTLRLDVQLSDTGDYLC-SLNDHLVGTVPVLLVDVPPPEPK 114
QY 118 VSC-QAADYENFSCWSPSQISGLPTRYLTSYRKTKVLGADSORRSPSTGPMPCP-QDPL 175
Db 115 LSCFRNLVNAICENRPSSTPS-PITKAVLFAKKI-----NTNGKSDQFVPCYSQQL 168
QY 176 GAARCVVHGAEFWSQYRI-NVTEVNPGLGASTRLDLVLSQSLRPPDPQGLRVESVPGYP 234
Db 169 KSPSCQVEILEGDKVHYVSLCVANSVGSKSHNEAFSLKWKQVDPDPANLVVSAIPGRP 228
QY 235 RGLRASWTYPASWPCQPHFLKFRLOYRPAQHPAWS-----TVEPAGLEEVIITDAVAGL 288
Db 229 RWLKVSQHPETWD-PSYLLQQLRYR-----PWSKEFTVLLPVAQYQCVIHDLRGV 283
QY 289 PHAVRVSARDFLDAGTWSTWSPAWCTPSTGTIPKEIPA---WGQLHTQPEVPEQVDSPA 345
Db 284 KHVVQVRGKEELDGLGQSEWSPVETGTPWIAE-PRITPAGILWNP--TQVSVE---DS-- 335
QY 346 PPRPSLQPHRLDHRD-----SVEQVAVILA-----SLGILSLGLVAGALGLW---- 392
Db 336 -----ANHEDQYESSTEATSVLAPVQESSMSLPTFL-VAGGSLAFGLLL 379
```

```
RESULT 5
I58141
ciliary neurotrophic factor receptor alpha chain - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I58141; A47387
R:Ip, N.Y.; McClain, J.; Barrezueta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, S.
Neuron 10, 89-102, 1993
A:Title: The alpha component of the CNTF receptor is required for signaling and defin
A:Reference number: I58141; MUID:93152175
A:Accession: I58141
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-372 <IPN>
A:Cross-references: GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056
R:Clatterbuck, R.E.; Price, D.L.; Koliatsos, V.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993
A:Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult
A:Reference number: A47387; MUID:93211934
A:Accession: A47387
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 185-260, 'D', 262-277 <CLA>
A:Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A:Experimental source: Sprague-Dawley, brain
A:Note: sequence extracted from NCBI backbone (NCBIN:128471, NCBIP:128472)
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C:Keywords: growth factor receptor
F:39-91/Domain: immunoglobulin homology <IMM>
F:116-296/Domain: cytokine receptor homology <CRS>

Query Match 16.4%; Score 374.5; DB 2; Length 372;
Best Local Similarity 31.5%; Pred. No. 1.2e-17;
Matches 112; Conservative 49; Mismatches 165; Indels 29; Gaps 13;

QY 1 MSSCSGLSRVLVAVATALVSASSPCQAWPGVQYQGPGRSVKLCPCGVTAGDPVSWF 60
Db 1 MAASVPWACCVALAAAVYTKHSPQE--APHVQVERIGTDTVTLPCGTASMDAAVTWR 58
QY 61 RDEPKLQGPDSGLGHELVLAQADSTDEGTTCQILDG-ALGCTVTLQLGYPARPVVS 119
Db 59 VNGTD---LAPDLNLSGLTLRLSLGLSHLYACFHRDHWLHRLHLLVGLPLPREVLS 115
QY 120 QCAADY-ENFSCWSPSQISGLPTRYLTSYRKTKVLGADSORRSPSTGPMPCPQDPLGAA 178
Db 116 CRSNTYKGFYCSNHLIS----APT-YIPNTFNVTVLHSGKM-----MVCEKDPALKN 162
QY 179 RCVVHGAEFWS--QYRINVTENVNPLGGASTRLDLVLSQSLRPPDPQGLRVESVPGYPRG 236
Db 163 RCHIRYMHLEFSTIKYKVSISVSNAL-GHNTAITDEFDEFTIKVDPDENNVVAVRVPSPNRR 221
QY 237 LRASWTYPASWPCQPHFLKFRLOYRPAQHPAWSVEPA-GLLEVITDAVAGLPHAVRVS 295
Db 222 LEVWTQTPSTWPDPEFPLKFFLYRPLDLDQWQHVLSNGTARTITDAYAGKEYIIQVA 281
QY 296 ARDFLDAGTWSTWSPAWCTPSTGTIPKEIPAWGQLHTQPEVPEQVDSPPAPRPS 350
Db 282 AKD-NEIGTWSWDSVAHAHATPWTEE-PRHLTTEAQ---APETTTSTSSSLAPPT 331

RESULT 6
S60614
growth promoting activity receptor alpha precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S60614
R:Heller, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer,
Development 121, 2681-2693, 1995
A:Title: Analysis of function and expression of the chick GPA receptor (GPARalpha) su
A:Reference number: S60614; MUID:95401882
A:Accession: S60614
A:Status: preliminary; nucleic acid sequence not shown
```


121 QAADYENFSCTWSPSQISGLPTRYLTSYRKKTVLGADSRSPSTGPWPCQDPLGA

AAR50326
 ID AAR50326 standard; Protein: 265 AA.
 XX
 AC AAR50326;
 XX
 DT 19-OCT-1994 (first entry)
 XX
 DE Mouse soluble EPO receptor protein fragment.
 XX
 KW Murine; soluble; erythropoietin; EPO; receptor protein; SEPO-R; drug;
 KW antigen; diagnostic agent; biochemical reagent.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT Protein /note= "Signal peptide"
 FT 26..265
 FT /note= "Mature EPO-R fragment"
 XX
 PN JP06038787-A.
 XX
 PD 15-FEB-1994.
 XX
 PF 04-MAR-1992; 92JP-0082865.
 XX
 PR 04-MAR-1992; 92JP-0082865.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 DR WPI; 1994-094847/12.
 DR N-PSDB; AAQ44853.
 XX
 PT Soluble erythropoietin receptor protein - and DNA coding for
 PT SEPO-R, useful as diagnostic reagent
 XX
 PS Disclosure; Page 5-6; 9pp; Japanese.
 XX
 CC This sequence represents a fragment of the murine soluble erythro-
 CC poietin (EPO) receptor protein (SEPO-R). This protein is able to
 CC bind to EPO and has antigenicity as an EPO receptor. The molecular
 CC weight of the full length protein is pref 33 or 29 kD. The protein
 CC is useful as a drug, as a diagnostic agent and a biochemical reagent.
 XX
 SQ Sequence 265 AA;

Query Match 96.8%; Score 30; DB 15; Length 265;
 Best Local Similarity 80.0%; Pred. NO. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WSXWS 5
 Db 232 wsaws 236

Search completed: August 24, 2001, 17:32:30
 Job time: 113 sec

QY 1 WSXWS 5
DB 200 wsaws 204

RESULT 13

AAB40915
ID AAB40915 standard; Protein; 221 AA.

AC AAB40915;

DT 08-FEB-2001 (first entry)

XX Human ORFX ORF679 polypeptide sequence SEQ ID NO:1358.

XX Human; open reading frame; ORFX: detection; cytostatic; hepatotropic;
KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antinflammatory disease; coagulation;
KW thrombosis; contraceptive.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

XX 02-APR-1999; 99US-0127636.

XX 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2000-602362/57.

XX N-PSDB; AAC75124.

XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -

XX Claim 11; Page 1158-1159; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,

CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.

SQ Sequence 221 AA;

Query Match 96.8%; Score 30; DB 21; Length 221;

Best Local Similarity 80.0%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5

DB 23 wsaws 27

RESULT 14

AAB21685

ID AAB21685 standard; peptide; 225 AA.

XX AAB21685;

XX 21-DEC-2000 (first entry)

DE Human mature erythropoietin receptor EPOR extracellular domain #1.

XX Ligand; cell surface receptor; erythropoietin; EPOR; human.

XX Homo sapiens.

XX WO200047612-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US03665.

XX 11-FEB-1999; 99US-0120009.

XX 29-APR-1999; 99US-0131674.

XX (XENC-) XENCOR INC.

XX Luo P, Dahiyat B;

XX WPI; 2000-549135/50.

XX Screening for ligand analogs and agents which modulate ligand-receptor

XX binding, comprises adding a test ligand to a non-naturally occurring

XX cell surface receptor analog -

XX Example 1; Fig 8; 82pp; English.

XX The present invention relates to a method for screening for a ligand
CC analog, comprising adding a candidate ligand to a non-naturally occurring
CC cell surface receptor analog e.g. erythropoietin receptor (EPOR), and
CC determining the binding of the ligand to the analog. The present sequence
CC is a mature human erythropoietin receptor (EPOR) extracellular domain.
CC This sequence may be used in the present invention as a cell surface
CC receptor analog.

XX Sequence 225 AA;

Query Match 96.8%; Score 30; DB 21; Length 225;

Best Local Similarity 80.0%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5

DB 209 wsaws 213

RESULT 15

XX (GETH) GENENTECH INC.
 XX Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ;
 PI Wells JA;
 XX WPI; 1992-096838/12.
 XX New method of modifying polypeptide hormone-receptor complex - to
 PT produce human growth hormone variant, useful for stimulating
 PT lactogenic and somatogenic response
 XX
 PS Disclosure; Page 41; 74pp; English.
 XX This truncated human prolactin binding protein is encoded by the
 CC insert contained in plasmid pPRLbp(1-211). The hPRLbp gene fragment
 CC is transcribed under the control of the alkaline phosphatase
 CC promoter and secreted into the host (E.coli) periplasm under the
 CC direction of the stII signal sequence. A stop codon and MluI
 CC restriction site were introduced after the threonine 211 codon which
 CC immediately precedes the transmembrane domain of the receptor. The
 CC plasmid was used as a template for site-directed mutagenesis to
 CC modify the metal-chelating centre of the protein. See, e.g. AAR24273
 CC for an example of a preferred variant.
 XX
 SQ Sequence 211 AA;

Query Match 96.8%; Score 30; DB 13; Length 211;
 Best Local Similarity 80.0%; Pred. NO. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WSXWS 5
 || ||
 Db 191 wsaws 195

RESULT 11
 AAR24273
 ID AAR24273 standard; Protein; 211 AA.

XX AC AAR24273;
 XX 20-JUL-1992 (first entry)
 XX Truncated human prolactin binding protein variant.
 XX hPRLbp; placental lactogen; zinc finger; chelate;
 KW receptor-ligand complex.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Misc-difference 188
 FT /note= "wild-type His replaced by Ala"

XX PN WO9203478-A.
 XX PD 05-MAR-1992.
 XX PF 16-AUG-1991; 91WO-US05856.
 XX PR 17-AUG-1990; 90US-0568936.

XX PA (GETH) GENENTECH INC.
 XX Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ;
 PI Wells JA;
 XX WPI; 1992-096838/12.

XX New method of modifying polypeptide hormone-receptor complex - to
 PT produce human growth hormone variant, useful for stimulating

PT lactogenic and somatogenic response
 XX Claim 41; Page 56; 74pp; English.
 XX Plasmid pPRLbp(1-211) (see AAR22228) coding for truncated, soluble
 CC prolactin binding protein was mutagenised such that the His codon
 CC at position 188 was substituted by an Ala codon. The hPRLbp variant
 CC has altered binding affinity for hGH.
 XX
 SQ Sequence 211 AA;

Query Match 96.8%; Score 30; DB 13; Length 211;
 Best Local Similarity 80.0%; Pred. NO. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WSXWS 5
 || ||
 Db 191 wsaws 195

RESULT 12
 AAB21686
 ID AAB21686 standard; peptide; 211 AA.

XX AC AAB21686;
 XX DT 21-DEC-2000 (first entry)
 XX Human mature erythropoietin receptor EPOR, extracellular domain #2.
 DE Ligand; cell surface receptor; erythropoietin; EPOR; human;
 KW protein design automation; PDA.
 XX OS Homo sapiens.

XX PN WO200047612-A2.
 XX PD 17-AUG-2000.
 XX PF 11-FEB-2000; 2000WO-US03665.
 XX PR 11-FEB-1999; 99US-0120009.
 XX PR 29-APR-1999; 99US-0131674.

XX PA (XENC-) XENCOR INC.
 XX Luo P, Dahiyat B;
 XX WPI; 2000-549135/50.

XX Screening for ligand analogs and agents which modulate ligand-receptor
 FT binding, comprises adding a test ligand to a non-naturally occurring
 FT cell surface receptor analog -

XX Example 1; Fig 8; 82pp; English.

XX The present invention relates to a method for screening for a ligand
 CC analog, comprising adding a candidate ligand to a non-naturally occurring
 CC cell surface receptor analog e.g. erythropoietin receptor (EPOR), and
 CC determining the binding of the ligand to the analog. The present sequence
 CC is a mature human erythropoietin receptor (EPOR) extracellular domain.
 CC Protein Design Automation was carried out on the present sequence, so
 CC that it may be used in the present invention as a cell surface receptor
 CC analog.

XX SQ Sequence 211 AA;

Query Match 96.8%; Score 30; DB 21; Length 211;
 Best Local Similarity 80.0%; Pred. NO. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PN WO200119860-A2.
 XX 22-MAR-2001.
 PD
 PF 14-SEP-2000; 2000WO-US25435.
 XX
 PR 15-SEP-1999; 99US-0154140.
 PR 06-DEC-1999; 99US-0169155.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 XX Tang YT, Hillman JL, Yue H, Reddy R, Lal P, Shah P, Azimzai Y;
 PI Baughn MR, Lu DAM, Bandman O, Shih LL, Patterson C;
 PI
 XX WPI: 2001-211447/21.
 DR N-PSDB; AAC85557.
 XX
 XX Isolated polypeptides and polynucleotides involved in cell
 PT differentiation are used for treatment, prevention and diagnosis of
 PT cell proliferative, developmental and neurological disorders e.g.
 PT cancer and Alzheimer's disease -
 XX
 XX Claim 1; Page 109; 137pp; English.
 PS
 XX The sequences given in ABA47123-50 show human polypeptides involved
 CC in cell differentiation (CDIFF). CDIFF polypeptides and agonists of
 CC these are used to treat a disease or condition associated with
 CC decreased expression of functional CDIFF. An antagonist of CDIFF is
 CC used to treat a disease or condition associated with over expression
 CC of functional CDIFF. CDIFF polypeptides may be used for the treatment,
 CC prevention and diagnosis of cell proliferative, developmental and
 CC neurological disorders, such as Alzheimer's disease, schizophrenic
 CC disorders, arteriosclerosis, cancer, atherosclerosis, diabetes mellitus
 CC and epilepsy. The CDIFF-16 sequence is homologous to Bos.taurus
 CC beta-A2 crystallin.
 XX
 XX Sequence 197 AA;
 SQ

Query Match 96.8%; Score 30; DB 22; Length 197;
 Best Local Similarity 80.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
 || ||
 Db 78 wsaws 82

RESULT 9
 AAB08135
 ID AAB08135 standard; Protein; 206 AA.
 XX
 AC AAB08135;
 XX
 XX 04-DEC-2000 (first entry)
 DT
 XX
 XX Amino acid sequence of a KIAA0550 polypeptide.
 DE
 XX
 XX Type 1 repeat; thrombospondin-1; TSP-1; Type 1 repeat peptide; TRP;
 KW KIAA0688; KIAA0550; angiogenesis inhibitor protein; angiogenesis;
 KW cancer; tumour; rheumatoid arthritis; psoriasis; retinopathy;
 KW ocular angiogenic disease; macular degeneration; corneal graft rejection;
 KW neovascular glaucoma; retrolental fibroplasia; rubecosis;
 KW Osler-Webber Syndrome; myocardial angiogenesis; haemophilic joint;
 KW plaque neovascularisation; telangiectasia; angiofibroma;
 KW wound granulation; coronary collateral; cerebral collateral;
 KW arteriovenous malformation; ischemic limb angiogenesis;
 KW neovascular glaucoma; retrolental fibroplasia; fracture; vasculogenesis;
 KW heliobacter related disease; hematopoiesis; ovulation; menstruation;
 KW placental; birth control; embryo implantation.
 XX
 XX Homo sapiens.
 OS

PN WO200047622-A2.
 XX 17-AUG-2000.
 PD
 PF 15-FEB-2000; 2000WO-GB00520.
 XX
 PR 15-FEB-1999; 99GB-0003408.
 PR
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 PA
 XX Mazarakis N, Martin-Rendon E, Kingsman SM;
 PI WPI: 2000-549137/50.
 DR
 XX Non-naturally occurring Type I repeat peptide (TRP) derived from human
 PT thrombospondin-1, KIAA0688 or KIAA0550 proteins, useful in the
 PT treatment of angiogenesis and/or cancer -
 PT
 XX Claim 5; Fig 7; 84pp; English.
 PS
 XX The present sequence represents a KIAA0550 polypeptide. The
 CC specification describes a non-naturally occurring Type I repeat peptide
 CC (TRP), derived from human thrombospondin-1 (HTSP-1), KIAA0688 or KIAA0550
 CC proteins. The TRP protein is an angiogenesis inhibitor protein. TRP
 CC proteins are used for the treatment of conditions associated with
 CC angiogenesis and cancer. Angiogenic mediated-diseases include tumours,
 CC rheumatoid arthritis, psoriasis, ocular angiogenic diseases, retinopathy
 CC of prematurity, macular degeneration, corneal graft rejection,
 CC neovascular glaucoma, retrolental fibroplasia, rubecosis), Osler-Webber,
 CC Syndrome, myocardial angiogenesis, plaque neovascularisation,
 CC telangiectasia, haemophilic joints, angiofibroma, wound granulation,
 CC coronary collaterals, cerebral collaterals, arteriovenous malformations,
 CC ischemic limb angiogenesis, neovascular glaucoma, retrolental
 CC fibroplasia, heliobacter related diseases, fractures, vasculogenesis,
 CC hematopoiesis, ovulation, menstruation and placental. TRPs are also
 CC useful in the treatment of disease of excessive or abnormal stimulation
 CC of endothelial cells. TRP can also be used as a birth control agent, as
 CC it prevents the vascularisation required for embryo implantation.
 XX
 XX Sequence 206 AA;
 SQ

Query Match 96.8%; Score 30; DB 21; Length 206;
 Best Local Similarity 80.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
 || ||
 Db 108 wsaws 112

RESULT 10
 AAR22228
 ID AAR22228 standard; protein; 211 AA.
 XX
 AC AAR22228;
 XX
 XX 20-JUL-1992 (first entry)
 DT
 XX Truncated human prolactin binding protein.
 DE
 XX hPRLbp; placental lactogen; zinc finger; chelate;
 KW receptor-ligand complex.
 KW
 XX Homo sapiens.
 OS
 XX WO9203478-A.
 PN
 XX 05-MAR-1992.
 PD
 XX 16-AUG-1991; 91WO-US05856.
 PF
 XX 17-AUG-1990; 90US-0568936.
 PR

DT 05-NOV-1992 (first entry)
 XX Partial MPLV-env related polypeptide.
 XX
 DE
 KW Myeloproliferative leukaemia virus; envelope protein; gp70;
 XX haematopoietic cell; Growth Factor receptor.
 XX
 OS Myeloproliferative leukaemia virus.
 XX
 XX W09207074-A.
 XX
 PD 30-APR-1992.
 XX
 XX 19-OCT-1990; 90WO-FR00762.
 XX
 XX 19-OCT-1990; 90WO-FR07623.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 XX Tambourin P, Varlet P, Vigon I, Wendling F;
 XX WPI; 1992-167154/20.
 DR N-PSDB; AAQ24676.
 XX
 XX Polypeptides similar to v-mlp protein of MPLV - for diagnosis and
 PT treatment of myeloproliferative diseases
 XX
 PS Claim 4; Page 31; 75pp; French.
 XX
 CC This polypeptide is an example of a fragment related to the MPLV
 CC env protein having the amino acid sequence assigned GENESEQ
 CC accession number AAR23970. The protein is involved in the
 CC ligand-fixing or signal-transmitting function of haematopoietic
 CC growth factor receptors; is recognised by antibodies to the
 CC protein AAR23970; when produced from the MPLV genome it can induce/
 CC promote proliferation of haematopoietic cells and/or is involved
 CC in differentiation of haematopoietic cells.
 CC See also AAQ24674-7.
 XX
 XX Sequence 184 AA;
 SQ

Query Match 96.8%; Score 30; DB 13; Length 184;
 Best Local Similarity 80.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 ||||
 Db 26 wsws 30

RESULT 7
 AAY18046
 ID AAY18046 standard; Protein; 190 AA.
 XX
 AC AAY18046;
 XX
 DT 03-AUG-1999 (first entry)
 XX
 DE Human mpl mutant protein sequence.
 XX
 KW Human; mpl; mutein; cytokine receptor; secretory signal; detection;
 KW extracellular region; membrane protein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX W09926978-A1.
 PN
 XX 03-JUN-1999.
 PD
 XX 26-NOV-1998; 98WO-JP05326.
 PF

XX 26-NOV-1997; 97JP-0324912.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA (KITA/) KITAMURA T.
 XX
 XX Kitamura T, Kojima T;
 PI
 XX WPI; 1999-347694/29.
 DR N-PSDB; AAX76826.
 XX
 PT DNA encoding human mpl fragment lacking secretory signal, is
 PT incorporated into a vector for detection of secretory proteins by
 PT induction of homeopoietic cell proliferation
 XX
 PS Claim 5; Page 24-26; 47pp; Japanese.
 XX
 CC This sequence is a human mpl mutant protein.
 CC The invention relates to a peptide derived from a cytokine receptor such
 CC as human mpl but lacking the secretory signal and most of the
 CC extracellular region. The invention also relates to a method for
 CC isolating cDNA encoding a secretory protein. The method is used for
 CC detection of secretory proteins (including type 1 and type 2 membrane
 CC proteins) in cDNA libraries.
 XX
 SQ Sequence 190 AA;
 XX

Query Match 96.8%; Score 30; DB 20; Length 190;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 ||||
 Db 29 wsws 33

RESULT 8
 AAB47135
 ID AAB47135 standard; Protein; 197 AA.
 XX
 AC AAB47135;
 XX
 DT 04-JUN-2001 (first entry)
 XX
 DE CDIFF-16, Incyte ID No. 3495166CDI.
 XX
 KW Human; cell differentiation; CDIFF; agonist; antagonist; epilepsy;
 KW cell proliferation; Alzheimer's disease; schizophrenic disorder;
 KW arteriosclerosis; cancer; atherosclerosis; diabetes mellitus.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH Modified-site 15
 FT /note= "Potential phosphorylation site"
 FT Modified-site 47
 FT /note= "Potential phosphorylation site"
 FT Modified-site 94
 FT /note= "Potential phosphorylation site"
 FT Modified-site 104
 FT /note= "Potential glycosylation site"
 FT Modified-site 109
 FT /note= "Potential phosphorylation site"
 FT Modified-site 142
 FT /note= "Potential phosphorylation site"
 FT Modified-site 176
 FT /note= "Potential phosphorylation site"
 FT Modified-site 177
 FT /note= "Potential phosphorylation site"
 FT Modified-site 191
 FT /note= "Potential phosphorylation site"
 XX

```
QY 1 WSXWS 5
DB 38 wsws 42

RESULT 4
AAB51501
ID AAB51501 standard; Protein; 48 AA.
XX
AC
XX
DT 16-FEB-2001 (first entry)
XX
DE Human secreted protein BLAST search protein SEQ ID NO: 178.
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200058495-A1.
XX
PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US07661.
XX
PR 26-MAR-1999; 99US-0126504.
PR 07-JAN-2000; 2000US-0174847.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-611720/58.
XX
PT New nucleic acid molecules encoding 45 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX
XX Disclosure; Page 404; 410pp; English.
XX
PS The invention relates to the isolation of genes AAC93310-C93354 encoding
PS the human secreted proteins AAB51380-B51423. The genes and proteins are
CC useful for preventing, ameliorating or treating medical conditions, e.g.
CC by protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment and
CC prevention of: (a) cancer, e.g. breast and ovarian cancer, and other
CC cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders
CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections. The present sequence is a protein isolated in the
CC present invention.
XX
SQ Sequence 48 AA;

Query Match 96.8%; Score 30; DB 21; Length 48;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 38 wsws 42

RESULT 5
AAY76592
ID AAY76592 standard; Protein; 82 AA.
XX
AC AAY76592;
XX
DT 10-APR-2000 (first entry)
XX
DE Human ovarian tumor EST fragment encoded protein 88.
KW Expressed sequence tag; EST; human; ovarian tumor; anticancer;
KW gene therapy; treatment.
XX
OS Homo sapiens.
XX
PN DE19817557-A1.
XX
PD 21-OCT-1999.
XX
PF 09-APR-1998; 98DE-1017557.
XX
PR 09-APR-1998; 98DE-1017557.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR WPI; 1999-591920/51.
DR N-PSDB; AAZ77487.
XX
XX New nucleic acid sequences expressed in ovarian, and some other, cancer
XX tissues, and derived polypeptides, for treatment of ovarian cancer and
XX identification of therapeutic agents.
XX
XX Claim 25; Page 279; 310pp; German.
XX
CC This invention describes novel nucleic acid (cDNA) sequences (A) which
CC have anticancer activity and are highly expressed in ovarian tumor
CC tissue (and some also in testis and breast cancer tissue). The products
CC of the invention can be used for gene therapy. (A) are used (i) for
CC recombinant expression of polypeptides (B) and (ii) to isolate complete
CC ovarian cancer; (ii) directly for treating this form of cancer
CC (including expression from gene therapy vectors) and (iii) for generation
CC of specific antibodies. (A) are identified by assembling ESTs (expressed
CC sequence tags) from a particular tissue type before comparison of
CC expression patterns. This allows a significantly longer fragment of the
CC gene to be revealed, so should reduce the number of failures associated
CC with the fact that ESTs from different libraries may represent different
CC parts of the same unknown gene, distorting the estimated frequency of
CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
CC fragments encoded by the human ovarian tumor cDNA library derived EST
CC fragments represented in AAZ77450-Z77572.
XX
SQ Sequence 82 AA;

Query Match 96.8%; Score 30; DB 20; Length 82;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 8 wsws 12

RESULT 6
AAR27660
ID AAR27660 standard; Protein; 184 AA.
XX
AC AAR27660;
XX
XX
```

PS Claim 8; Page 63; 67pp; English.

XX The peptides AAR69780-90 are active peptide fragments based on the
CC second type 1 repeat sequence (amino acids 412-473) of thrombospondin
CC (sequence not given in the specification) which can be used to inhibit
CC the stimulation of transforming growth factor-beta (TGF- β) from latent
CC TGF- β . The inhibitory peptides can be used to prevent fibrosis or block
CC TGF- β mediated endothelial cell proliferation. Peptides (see
CC AAR69766-79) which stimulate the conversion of latent TGF- β to active
CC TGF- β can be used to enhance wound healing.

XX Sequence 5 AA;

Query Match 96.8%; Score 30; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 1 WSSWS 5

RESULT 2
AAR98939

ID AAR98939 standard; peptide; 32 AA.

AC AAR98939;

DT 28-SEP-1996 (first entry)

DE Synthetic human erythropoietin receptor peptide, SE-9.

KW Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;
KW erythropoiesis; erythrocyte production; epitope mapping.

XX Synthetic.

PN WO9603438-A1.

PD 08-FEB-1996.

PF 26-JUL-1995; 95WO-US09458.

PR 26-JUL-1994; 94US-0280864.

PA (AMGE-) AMGEN INC.

XX Elliott SG;

DR WPI; 1996-117004/12.

XX Monoclonal antibodies stimulating an erythropoietin receptor -
PT useful in diagnosis and treatment of patients having disorders
PT associated with low red blood cell levels, e.g. anaemia

PS Example 6; Page 34; 61pp; English.

XX AAR9960-R9965 and AAR98936-R98939 are overlapping, synthetic human
CC erythropoietin receptor (shuEPOR) peptides which span residues 1 to
CC 244 of the human EPOR. The peptides are used to map the EPOR binding
CC epitope of an EPOR monoclonal antibody which binds to EPORs and
CC stimulates erythropoiesis by stimulating the proliferation and/or
CC differentiation of erythroid progenitor cells to erythrocytes.
CC Pharmaceutical compns. contg. the antibody may be used in the
CC diagnosis and treatment of patients having disorders associated with
CC low red blood cell levels, e.g. anaemia. The antibodies are also
CC useful in methods and kits for detecting EPORs in biological in
CC biological samples.

XX Sequence 32 AA;

Query Match 96.8%; Score 30; DB 21; Length 48;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.8%; Score 30; DB 17; Length 32;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 16 WSAWS 20

RESULT 3

AAB51497
ID AAB51497 standard; Protein; 48 AA.

XX AAB51497;

DT 16-FEB-2001 (first entry)

DE Human secreted protein BLAST search protein SEQ ID NO: 174.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.

OS Homo sapiens.

XX WO200058495-A1.

PD 05-OCT-2000.

PF 23-MAR-2000; 2000WO-US07661.

PR 26-MAR-1999; 95US-0126504.

PR 07-JAN-2000; 2000US-0174847.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

DR WPI; 2000-611720/58.

XX New nucleic acid molecules encoding 45 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -

PS Disclosure; Page 402; 410pp; English.

XX The invention relates to the isolation of genes AAC93310-C93354 encoding
CC the human secreted proteins AAB51380-B51423. The genes and proteins are
CC useful for preventing, ameliorating or treating medical conditions, e.g.
CC by protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment and
CC prevention of: (a) cancer, e.g. breast and ovarian cancer, and other
CC cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders
CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections. The present sequence is a protein isolated in the
CC present invention.

XX Sequence 48 AA;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2001, 17:30:37 ; Search time 32.57 Seconds
(without alignments)
9.307 Million cell updates/sec

Title: US-09-532-263-1
Perfect score: 31
Sequence: 1 WSXWS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	5	16	Thrombospondin-der
2	30	96.8	32	17	Synthetic human er
3	30	96.8	48	21	Human secreted pro
4	30	96.8	48	21	Human secreted pro
5	30	96.8	82	20	Human ovarian tumo
6	30	96.8	184	13	Partial MPLV-env r
7	30	96.8	190	20	Human mpl mutant p
8	30	96.8	197	22	CDIFF-16, Incyte I
9	30	96.8	206	21	Amino acid sequenc
10	30	96.8	211	13	Truncated human pr
11	30	96.8	211	13	Truncated human pr

12	30	96.8	211	21	Human mature eryth
13	30	96.8	221	21	Human ORFX ORF679
14	30	96.8	225	21	Human mature eryth
15	30	96.8	265	15	Mouse soluble EPO
16	30	96.8	284	13	MPLV env-vmpl fusi
17	30	96.8	334	20	Human.mpl-GM-CSF f
18	30	96.8	334	20	Human.mpl-GM-CSF f
19	30	96.8	349	21	Soluble human prol
20	30	96.8	349	21	Human prolactin re
21	30	96.8	370	22	C. elegans UNC-5 p
22	30	96.8	379	21	Murine soluble int
23	30	96.8	380	21	Arabidopsis thalia
24	30	96.8	380	21	Arabidopsis thalia
25	30	96.8	382	13	MPLV-env related p
26	30	96.8	385	21	Arabidopsis thalia
27	30	96.8	397	21	Arabidopsis thalia
28	30	96.8	397	21	Arabidopsis thalia
29	30	96.8	400	12	Human GM-CSF recep
30	30	96.8	415	21	Breast and ovarian
31	30	96.8	422	17	Human interleukin-
32	30	96.8	422	22	Human IL-11 recept
33	30	96.8	423	17	Human interleukin-
34	30	96.8	432	17	Murine interleukin
35	30	96.8	432	22	Mouse IL-11 recept
36	30	96.8	438	21	Truncated human Ep
37	30	96.8	438	21	R154C truncated hu
38	30	96.8	441	17	Murine Etl-2 gene
39	30	96.8	482	16	Soluble murine MPL
40	30	96.8	488	18	EpoRfc fusion prot
41	30	96.8	503	21	Q-tagged erythropo
42	30	96.8	507	11	EPO receptor sequ
43	30	96.8	507	15	MEL EPO receptor.
44	30	96.8	507	15	Mouse soluble EPO
45	30	96.8	507	16	Mouse erythropoiet

ALIGNMENTS

RESULT 1
AAR69782
ID AAR69782 standard; peptide; 5 AA.
XX
AC AAR69782;
XX
DT 13-OCT-1995 (first entry)
XX
DE Thrombospondin-derived TGF-beta inhibitory peptide #2.
XX
KW Thrombospondin type 1 repeat sequence; transforming growth factor-beta;
KW wound healing; fibrosis; endothelial cell proliferation.
XX
OS Synthetic.
XX
PN W09505191-A.
XX
PD 23-FEB-1995.
XX
PF 12-AUG-1994; 94WO-US09193.
XX
PR 13-AUG-1993; 93US-0106120.
PR 04-MAY-1994; 94US-0238169.
XX
(UABR-) UAB RES FOUND.
XX
PI Krutzsch HC, Murphy-Ullrich JE, Roberts DD, Schultz-Cherry S;
XX
DR WPI; 1995-098579/13.
XX
PT Stimulating or inhibiting transforming growth factor-beta by
PT contacting with thrombospondin or an activating enzyme - used
PT to enhance wound healing or prevent fibrosis
XX

THIS PAGE BLANK (USPTO)

CC -!- FUNCTION: A POSITIVE REGULATOR OF THE ALTERNATE PATHWAY OF
CC COMPLEMENT. IT BINDS TO AND STABILIZES THE C3-AND C5-CONVERTASE
CC ENZYME COMPLEXES.
CC
CC -!- SIMILARITY: CONTAINS 6 TSP TYPE-1 DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X12905; CAA31389.1; -
CC DR PIR; S05478; S05478.
CC DR MGD; MGI:104724; Fdxr.
CC DR InterPro: IPR000884; -
CC DR Pfam; PF00090; tsp_1; 6.
CC DR PROSITE; PS50092; TSP1; 6.
CC KW Complement alternate pathway; Glycoprotein; Repeat.
CC FT NON_TER 1 1
CC FT DOMAIN 46 103 TSP TYPE-1 1.
CC FT DOMAIN 104 160 TSP TYPE-1 2.
CC FT DOMAIN 161 224 TSP TYPE-1 3.
CC FT DOMAIN 225 282 TSP TYPE-1 4.
CC FT DOMAIN 283 345 TSP TYPE-1 5.
CC FT DOMAIN 346 405 TSP TYPE-1 6.
CC FT CARBOHYD 396 396 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 437 AA; 47538 MW; 2B8DBCE22B3B78BE CRC64;

Query Match 96.8%; Score 30; DB 1; Length 437;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSXWS 5
DB 49 WSAWS 53

RESULT 15
ADRO_MOUSE
ID ADRO_MOUSE STANDARD; PRT; 494 AA.
AC Q61578;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR
DE (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)
DE REDUCTASE).
GN FDXR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RX MEDLINE=96085117; PubMed=7495857;
RA Itoh S., Iemura O., Yamada E., Yoshimura T., Tsujikawa K., Kohama Y.,
RA Mimura T.;
RT "cDNA cloning of mouse ferredoxin reductase from kidney.";
RL Biochim. Biophys. Acta 1264:159-162(1995).
CC -!- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE
CC MITOCHONDRIAL P450 SYSTEMS. INCLUDING CHOLESTEROL SIDE CHAIN
CC CLEAVAGE IN ALL STEROIDGENIC TISSUES, STEROID 11-BETA
CC HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24
CC HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE
CC LIVER.
CC -!- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED
CC ADRENODOXIN + NADPH.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.

CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE ADRENAL, TESTIS AND OVARY AND
CC TO A LESSER EXTENT IN THE LIVER AND KIDNEY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D49920; BAA08659.1; -
CC DR MGD; MGI:104724; Fdxr.
CC DR InterPro: IPR000759; -
CC DR PRINTS; PR00419; ADXRDTASE.
CC KW Electron transport; Oxidoreductase; Flavoprotein; NADP; FAD;
CC KW Mitochondrion; Transit peptide.
CC FT TRANSIT 1 34
CC FT CHAIN 35 494 MITOCHONDRION (POTENTIAL).
CC SQ SEQUENCE 494 AA; 54202 MW; 4BD279DFC606A5C5 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 494;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSXWS 5
DB 11 WSAWS 15

Search completed: August 24, 2001, 17:34:32
Job time: 160 sec

```

DR EMBL; M64445; AAA35908.1; -
DR EMBL; X54935; CAA38697.1; -
DR EMBL; M73832; AAA35909.1; -
DR EMBL; L29348; AAA60961.1; -
DR EMBL; L29349; AAA60962.1; -
DR EMBL; U93096; AAB51535.1; -
DR PIR; S06945; S06945.
DR MIM; M6250; -
DR MIM; M42500; -
DR InterPro; IPR000950; -
DR InterPro; IPR002465; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 22
FT CHAIN 23 400
FT FT 23 320
FT FT 320 320
FT DOMAIN 23 320
FT TRANSMEM 321 346
FT DOMAIN 347 400
FT DISULFID 126 136
FT DISULFID 165 178
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 99 99
FT CARBOHYD 123 123
FT CARBOHYD 135 135
FT CARBOHYD 182 182
FT CARBOHYD 195 195
FT CARBOHYD 223 223
FT CARBOHYD 229 229
FT CARBOHYD 272 272
FT CARBOHYD 305 305
FT VARSPIC 216 233
FT FT 234 400
FT VARSPIC 271 286
FT FT 287 400
FT VARSPIC 316 400
FT FT 318 333
FT VARSPIC 334 400
FT VARSPIC 376 400
FT FT 400 AA; 46206 MW; D9025B981E41311D CRC64;
SQ SEQUENCE 400 AA; 46206 MW; D9025B981E41311D CRC64;

Query Match 96.8%; Score 30; DB 1; Length 400;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 306 WSSWS 310

RESULT 13
ERR1_YEAST
ID ERR1_YEAST STANDARD; PRT; 437 AA.
AC P42222;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ENOLASE RELATED PROTEIN 1 (EC 4.2.1.11).
GN ERR1 OR YMR323W OR YW924.15.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

```

```

RN SEQUENCE FROM N.A.
RP STRAIN=S288C / AB972;
RA Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 120-437 FROM N.A.
RP STRAIN=S288C / YPI;
RC STRAIN=S288C / YPI;
RX Pryde F.E., Huckle T.C., Louis E.J.;
RT "Sequence analysis of the right end of chromosome XV in Saccharomyces
RT cerevisiae: an insight into the structural and functional
RT significance of sub-telomeric repeat sequences."
RL Yeast 11:371-382(1995).
CC 1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2O).
CC 1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z54141; CAA90841.1; -
CC EMBL; U23472; AAC48992.1; -
CC HSSP; P00924; INEL.
CC SGD; S0005920; ERRI.
CC InterPro; IPR000941; -
CC Pfam; PF00113; enolase; 1.
CC PRINTS; PR00148; ENOLASE.
CC PROSITE; PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium.
FT ACT_SITE 160 160 BY SIMILARITY.
FT METAL 247 247 MAGNESIUM (BY SIMILARITY).
FT METAL 296 296 MAGNESIUM (BY SIMILARITY).
FT METAL 321 321 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 437 AA; 47312 MW; 143D6EF66FB03D13 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 437;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 304 WSSWS 308

RESULT 14
PROP_MOUSE
ID PROP_MOUSE STANDARD; PRT; 437 AA.
AC P11680;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROPERDIN (FRAGMENT).
GN PFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=88318954; PubMed=3045564;
RA Goundis A., Reid K.B.M.;
RT "Properdin, the terminal complement components, thrombospondin and
RT the circumsporozoite protein of malaria parasites contain similar
RT sequence motifs."
RN Nature 335:82-85(1988).

```


Proc. Natl. Acad. Sci. U.S.A. 82:4356-4359(1985).
 -!- SUBCELLULAR LOCATION: SECRETED.
 CC DEVELOPMENTAL STAGE: PLACENTAL LACTOGEN I IS EXPRESSED IN MID-
 CC PREGNANCY, WHILE PLACENTAL LACTOGEN II IS EXPRESSED THROUGHOUT
 CC THE LATER HALF OF PREGNANCY.
 CC -!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M14647; AAA39947.1; -;
 DR EMBL; M85066; AAA75165.1; -;
 DR EMBL; M85062; AAA75165.1; JOINED.
 DR EMBL; M85063; AAA75165.1; JOINED.
 DR EMBL; M85064; AAA75165.1; JOINED.
 DR PIR; A26489; A26489.
 DR PIR; A44090; A44090.
 DR HSSP; Q28632; LAN3.
 DR MGD; MGI:97607; P12.
 DR InterPro; IPR001400; -;
 DR Pfam; PF00103; hormone; 1.
 DR PRINTS; PR00836; SOMATOTROPIN.
 DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
 DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
 KW Hormone; Placenta; Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 222 PLACENTAL LACTOGEN II.
 FT DISULFID 82 197 BY SIMILARITY.
 FT DISULFID 214 222 BY SIMILARITY.
 FT CONFLICT 101 160 MISSING (IN REF. 2).
 SQ SEQUENCE 222 AA; 25159 MW; 5A0D19D03D76EB05 CRC64;
 Query Match 96.8%; Score 30; DB 1; Length 222;
 Best Local Similarity 80.0%; Pred No. 1;le02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WSXWS 5
 Db 173 WSAWS 177
 RESULT 12
 GPCR_HUMAN
 ID GPCR_HUMAN STANDARD; PRT; 400 AA.
 AC P15509; Q14429; Q14430; Q14431; Q00207; Q16564;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA
 DE CHAIN PRECURSOR (GM-CSF-R-ALPHA) (GMR) (CDW116) (CD116 ANTIGEN).
 GN CSF2RA OR CSF2R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Placenta;
 RX MEDLINE=90059966; PubMed=2555171;
 RA Gearing D.P., King J.A., Gough N.M., Nicola N.A.;
 RT "Expression cloning of a receptor for human granulocyte-macrophage
 RT colony-stimulating factor.";
 RL EMBO J. 8:3667-3676(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=94193800; PubMed=8144676;
 RA Nakagawa Y., Kosugi H., Miyajima A., Arai K.I., Yokota T.;

RT "Structure of the gene encoding the alpha subunit of the human
 RT granulocyte-macrophage colony stimulating factor receptor.
 RT Implications for the evolution of the cytokine receptor
 RT superfamily.";
 RL J. Biol. Chem. 269:10905-10912(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=91352066; PubMed=1715577;
 RA Crosier K.E., Wong G.G., Mathey-Prevot B., Nathan D.G., Sieff C.A.;
 RT "A functional isoform of the human granulocyte/macrophage colony-
 RT stimulating factor receptor has an unusual cytoplasmic domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7744-7748(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Placenta;
 RX MEDLINE=91088339; PubMed=2148207;
 RA Ashworth A., Kraft A.;
 RT "Cloning of a potentially soluble receptor for human GM-CSF.";
 RL Nucleic Acids Res. 18:7178-7178(1990).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=91376112; PubMed=1832774;
 RA Raines M.A., Liu L., Quan S.G., Joe V., DiPersio J.F., Golde D.W.;
 RT "Identification and molecular cloning of a soluble human granulocyte-
 RT macrophage colony-stimulating factor receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
 RC TISSUE=Blood;
 RX MEDLINE=94368898; PubMed=8086503;
 RA Hu X., Emanuel P.D., Zuckerman K.S.;
 RT "Cloning and sequencing of the cDNA encoding two alternative
 RT splicing-derived variants of the alpha subunit of the granulocyte-
 RT macrophage colony-stimulating factor receptor.";
 RL Biochim. Biophys. Acta 1223:306-308(1994).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RA Hu X., Zuckerman K.S.;
 RT "Cloning and sequencing of the cDNA variant with 397 bp missing
 RT for the GM-CSF receptor alpha subunit.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-
 CC STIMULATING FACTOR. TRANSDUCES A SIGNAL THAT RESULTS IN THE
 CC PROLIFERATION, DIFFERENTIATION, AND FUNCTIONAL ACTIVATION OF
 CC HEMATOPOIETIC CELLS.
 CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORMS 3, 4 AND 6
 CC ARE PROBABLY SOLUBLE.
 CC -!- ALTERNATIVE PRODUCTS: 6 ISOFORMS: 1 (SHOWN HERE), 2, 3, 4, 5 AND
 CC 6; ARE PRODUCED BY ALTERNATIVE SPLICING
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X17648; CAA35638.1; -;
 DR EMBL; D26628; BAA05656.1; -;
 DR EMBL; D26618; BAA05656.1; JOINED.
 DR EMBL; D26619; BAA05656.1; JOINED.
 DR EMBL; D26620; BAA05656.1; JOINED.
 DR EMBL; D26621; BAA05656.1; JOINED.
 DR EMBL; D26622; BAA05656.1; JOINED.
 DR EMBL; D26623; BAA05656.1; JOINED.
 DR EMBL; D26624; BAA05656.1; JOINED.
 DR EMBL; D26625; BAA05656.1; JOINED.
 DR EMBL; D26626; BAA05656.1; JOINED.
 DR EMBL; D26627; BAA05656.1; JOINED.

```
QY 1 WSXWS 5
DB 77 WSAWS 81

RESULT 9
CRBB_MOUSE
ID CRBB_MOUSE STANDARD; PRT; 196 AA.
AC Q9JVV1;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BETA CRYSTALLIN A2 (BETA-A2-CRYSTALLIN).
GN CRYBA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RN GRAY J.;
RT "Sequence analysis of beta-A2-, beta-A4- and beta-B3-crystallin cDNA
RT completes the identification of the members of this gene family in the
RT mouse."
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -1- SUBUNIT: HOMO/ETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ272227; CAB75585.1; -
DR MGD; MGI:104336; Cryba2.
DR InterPro; IPR001064; -
DR Pfam; PF00030; crystall; 2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 3.
KW Eye lens protein; Duplication.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 10 N-TERMINAL ARM.
FT DOMAIN 11 51 MOTIF 1.
FT DOMAIN 52 99 MOTIF 2.
FT DOMAIN 100 104 CONNECTING PEPTIDE.
FT DOMAIN 105 146 MOTIF 3.
FT DOMAIN 147 196 MOTIF 4.
SQ SEQUENCE 196 AA; 22105 MW; A02FD7583005D14E CRC64;

Query Match 96.8%; Score 30; DB 1; Length 196;
Best Local Similarity 80.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 77 WSAWS 81

RESULT 10
ALBR_KLEOX
ID ALBR_KLEOX STANDARD; PRT; 218 AA.
AC P10488;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)

Query Match 96.8%; Score 30; DB 1; Length 196;
Best Local Similarity 80.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 77 WSAWS 81

RESULT 11
PLC2_MOUSE
ID PLC2_MOUSE STANDARD; PRT; 222 AA.
AC P09586;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PLACENTAL LACTOGEN II PRECURSOR (PL-II).
GN PL2 OR PL-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RN MEDLINE=87041482; PubMed=3464966;
RX Jackson L.L., Colosi P., Talamantes F., Linzer D.I.H.;
RT "Molecular cloning of mouse placental lactogen cDNA."
RT Proc. Natl. Acad. Sci. U.S.A. 83:8496-8500(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92237269; PubMed=1570305;
RX Shida M.M., Jackson-Grusby L.L., Ross S.R., Linzer D.I.H.;
RT "Placental-specific expression from the mouse placental lactogen II
RT gene promoter."
RT Proc. Natl. Acad. Sci. U.S.A. 89:3864-3868(1992).
RN [3]
RP SEQUENCE OF 32-50.
RX MEDLINE=85242883; PubMed=3859888;
RX Linzer D.I.H., Lee S.-J., Orgren L., Talamantes F., Nathans D.;
RT "Identification of proliferin mRNA and protein in mouse placenta."
RT
```

```

RESULT 7
CRBB_BOVIN
ID CRBB_BOVIN STANDARD; PRT; 196 AA.
AC P26444.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BETA CRYSTALLIN A2 (BETA-A2-CRYSTALLIN).
GN CRYBA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RX MEDLINE=91340151; PubMed=1874445;
RA van Rens G.L., Driessen H.P.C., Nalini V., Slingsby C., de Jong W.W.,
RT Bloemendal H.;
RT "Isolation and characterization of cDNAs encoding beta A2- and beta
RT A4-crystallins: heterologous interactions in the predicted beta
RT A4-beta B2 heterodimer.";
RL Gene 102:179-188(1991).
RN [2]
RP SEQUENCE OF 133-196.
RC TISSUE=Lens cortex;
RX MEDLINE=84132067; PubMed=6698025;
RA Berbers G.A.M., Hoekman W.A., Bloemendal H., de Jong W.W.,
RA Kleinschmidt T., Braunlitzer G.;
RT "Homology between the primary structures of the major bovine beta-
RT crystallin chains.";
RL Eur. J. Biochem. 139:467-479(1984).
CC -!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -!- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60329; AAA30402.1; .
DR PIR; D27898.
DR PIR; JH0602; JH0602.
DR HSP; P02522; IBLB.
DR InterPro; IPR001064; .
DR Pfam; PF00030; Crystall; 2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 3.
KW Eye lens protein; Duplication.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 10 N-TERMINAL ARM.
FT DOMAIN 11 51 MOTIF 1.
FT DOMAIN 52 99 MOTIF 2.
FT DOMAIN 100 104 CONNECTING PEPTIDE.
FT DOMAIN 105 146 MOTIF 3.
FT DOMAIN 147 196 MOTIF 4.
FT CONFLICT 182 184 QAH -> HAQ (IN REF. 2).
SQ SEQUENCE 196 AA; 22099 MW; B694586F8903B47F CRC64;

```

Query Match 96.8%; Score 30; DB 1; Length 196;
 Best Local Similarity 80.0%; Pred. No. 97;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 WSXWS 5
DB 77 WSAWS 81

RESULT 8
CRBB_HUMAN
ID CRBB_HUMAN STANDARD; PRT; 196 AA.
AC P53672; Q9Y562;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BETA CRYSTALLIN A2 (BETA-A2-CRYSTALLIN).
GN CRYBA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Wistow G.;
RX Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 108-141 AND 157-184 FROM N.A.
RX MEDLINE=96039268; PubMed=7490092;
RA Hulsebos T.J.M., Cerosaletti K.M., Fournier R.E.K., Sinke R.J.,
RA Rocchi M., Marzella R., Jenkins N.A., Gilbert N.C., Copeland N.G.;
RT "Identification of the human beta A2 crystallin gene (CRYBA2):
RT localization of the gene on human chromosome 2 and of the homologous
RT gene on mouse chromosome 1.";
RL Genomics 28:543-548(1995).
CC -!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -!- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF166331; AAD45388.1; .
DR EMBL; X86395; CAA60147.1; .
DR EMBL; X86396; CAA60148.1; .
DR HSP; P02522; IBLB.
DR MIM; 600836; .
DR InterPro; IPR001064; .
DR Pfam; PF00030; Crystall; 2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 3.
KW Eye lens protein; Duplication.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 10 N-TERMINAL ARM.
FT DOMAIN 11 51 MOTIF 1.
FT DOMAIN 52 99 MOTIF 2.
FT DOMAIN 100 104 CONNECTING PEPTIDE.
FT DOMAIN 105 146 MOTIF 3.
FT DOMAIN 147 196 MOTIF 4.
FT CONFLICT 116 116 Q -> L (IN REF. 2).
SQ SEQUENCE 196 AA; 21964 MW; F92FEE924844DF51 CRC64;

```

Query Match 96.8%; Score 30; DB 1; Length 196;
 Best Local Similarity 80.0%; Pred. No. 97;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RA Brandon R.C., Rogers V.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Balles R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*,"
 RA Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE OF 62-142 FROM N.A.
 RC STRAIN-CANTON-S;
 RX MEDLINE=94211204; PubMed=8159165;
 RA Daffre S., Kylsten P., Samakovlis C., Hultmark D.,
 RT "The lysozyme locus in *Drosophila melanogaster*: an expanded gene
 RT family adapted for expression in the digestive tract.";
 RL Mol. Gen. Genet. 242:152-162(1994).
 CC -1- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
 CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
 CC FOOD. MAY BE INVOLVED IN THE CLEARANCE OF BACTERIA FROM THE LARVAL
 CC GUT BEFORE METAMORPHOSIS.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
 CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYL-MURAMIC ACID IN PEPTIDOGLYCAN
 CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.
 CC -1- DEVELOPMENTAL STAGE: RISES DRAMATICALLY IN THE LATE THIRD INSTAR,
 CC THEN DECREASES GRADUALLY DURING THE PUPAL STAGES. LOW EXPRESSION
 CC IS FOUND IN ADULTS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: A5003470; AAF47445.1; -
 CC EMBL: Z22224; CAA80226.1; -
 CC PIR: S32650; S32650.
 CC HSP: P00698; IAT6.
 CC FlyBase: FBgn0004431; Lysx.
 CC InterPro: IPR001916; -
 CC Pfam: PF00062; lys; 1.
 CC PROSITE: PS00128; LACTALBUMIN_LYSOZYME; 1.
 KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;
 KW Multigene family.

FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 142 LYSOZYME X.
 FT DISULFID 25 140 BY SIMILARITY.
 FT DISULFID 46 130 BY SIMILARITY.
 FT DISULFID 81 97 BY SIMILARITY.
 FT DISULFID 93 111 BY SIMILARITY.
 FT ACT_SITE 51 51 BY SIMILARITY.
 FT ACT_SITE 69 69 BY SIMILARITY.
 FT CONFLICT 78 78 M -> L (IN REF. 2).
 SQ SEQUENCE 142 AA; 15591 MW; 2A48035364B995B8C CRC64;
 Query Match 96.8%; Score 30; DB 1; Length 142;
 Best Local Similarity 80.0%; Pred. No. 73;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WSXWS 5
 DB 121 WSAWS 125
 ID MPL_MPLV STANDARD; PRT; 184 AA.
 AC P40931;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MYELOPROLIFERATIVE LEUKEMIA PROTEIN.
 DE V-MPL.
 GN Myeloproliferative leukemia virus (MPLV).
 OS Viruses; Retroviridae.
 OX NCBI_TaxID=11973;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91084843; PubMed=2175677;
 RA Souyri M., Vigon I., Penciolelli J.-F., Heard J.-M., Tambourin P.,
 RA Wendling F.;
 RT "A putative truncated cytokine receptor gene transduced by the
 RT myeloproliferative leukemia virus immortalizes hematopoietic
 RT progenitors.";
 RL Cell 63:1137-1147(1990).
 CC -1- FUNCTION: TRUNCATED FORM OF THE RECEPTOR FOR THROMBOPOIETIN.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-MPL
 CC POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M50350; AAA77654.1; -
 CC HSP: P19235; 1EBP.
 CC PROSITE: PS01352; HEMATOPO_REC_L_F1; PARTIAL.
 CC InterPro: IPR000950; -
 CC InterPro: IPR002465; -
 CC Receptor; Transmembrane; Oncogene.
 FT TRANSMEM 44 64 POTENTIAL.
 SQ SEQUENCE 184 AA; 20558 MW; 7986D3363940B735 CRC64;
 Query Match 96.8%; Score 30; DB 1; Length 184;
 Best Local Similarity 80.0%; Pred. No. 92;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WSXWS 5
 DB 26 WSAWS 30

```

QY 1 WSXWS 5
   11 11
Db 120 WSAWS 124

RESULT 4
LYSE_DROME
ID LYSE_DROME STANDARD: PRT: 140 AA.
AC P37159; Q9W0J5;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYSE_DROME PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLURAMIDASE E).
GN LYSE OR CG1180.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=94211204; PubMed=8159165;
RA Daffre S., Kylisten P., Samakowis C., Hultmark D.;
RT "The lysozyme locus in Drosophila melanogaster: an expanded gene
RL family adapted for expression in the digestive tract.";
RN Mol. Gen. Genet. 242:152-162(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazew R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimios I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
CC FOOD.

```

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
 N-ACETYL-D-GLUCOSAMINE AND N-ACETYLURAMIC ACID IN PEPTIDOGLYCAN
 HETEROOLYMERS OF THE PROKARYOTES CELL WALLS.
 -!- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.
 -!- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD
 LARVAL INSTAR, IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL
 STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
 SECOND LARVAL INSTARS.
 -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

EMBL; 222227; CAA80229.1; -;
 EMBL; AE003470; AAF47451.1; -;
 PIR; S32634; S32634.
 HSSP; P11941; LLMC.
 DR. FlyBase; FBgn0004428; Lyse.
 InterPro; IPR001916; -;
 Pfam; PF00062; lys; 1.
 DR PROSITE; PS00128; LACTALBUMIN_LYSOZYME; 1.
 KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;
 MW Multigene family.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT CHAIN 19 140 LYSOZYME E.
 FT DISULFID 24 139 BY SIMILARITY.
 FT DISULFID 45 129 BY SIMILARITY.
 FT DISULFID 80 96 BY SIMILARITY.
 FT DISULFID 92 110 BY SIMILARITY.
 FT ACT_SITE 50 50 BY SIMILARITY.
 FT ACT_SITE 68 68 BY SIMILARITY.
 FT CONFLICT 12 12 M -> L (IN REF. 1).
 FT CONFLICT 76 76 N -> D (IN REF. 1).
 FT CONFLICT 138 138 G -> D (IN REF. 1).
 SQ SEQUENCE 140 AA; 15552 MW; CEB5465CF6B6F123 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 140;
 Best Local Similarity 80.0%; Pred. No. 73;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 120 WSAWS 124

RESULT 5
 LYSE_DROME STANDARD: PRT: 142 AA.
 AC P37161; Q9W0K1;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LYSOZYME X PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLURAMIDASE X).
 GN LYSE OR CG9120.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

CC EMBL; 222225; CAA80227.1; -
 CC EMBL; AE003470; AAF47448.1; -
 CC PIR; S32620; S32620.
 CC PIR; S32643; S32643.
 CC HSP; P11941; 1LMC.
 CC FlyBase; FBgn0004425; LysB.
 CC InterPro; IPR000974; -
 CC InterPro; IPR001916; -
 CC Pfam; PF00062; Lys; 1.
 CC PROSITE; PS00128; LACTALBUMIN_LYSOZYME; 1.
 CC HydroLase; Glycosidase; Bacteriolytic enzyme; Signal;
 KW Multigene family.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT CHAIN 19 140 LYSOZYME B.
 FT DISULFID 24 139 BY SIMILARITY.
 FT DISULFID 45 129 BY SIMILARITY.
 FT DISULFID 80 96 BY SIMILARITY.
 FT DISULFID 92 110 BY SIMILARITY.
 FT ACT_SITE 50 50 BY SIMILARITY.
 FT ACT_SITE 68 68 BY SIMILARITY.
 FT CONFLICT 12 13 LA -> SG (IN REF. 1).
 FT SEQUENCE 140 AA; 15611 MW; 70AFA5321857F093 CRC64;
 SQ

Query Match 96.8%; Score 30; DB 1; Length 140;
 Best Local Similarity 80.0%; Pred. No. 73;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 |||||
 Db 120 WSAWS 124

RESULT 3
 LYSB_DROME STANDARD; PRT; 140 AA.
 AC P29614; Q9W0J6;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LYSOZYME D PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLGLUCOSAMINIDASE D).
 GN LYSB OR CG9118.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RX MEDLINE=92269751; PubMed=1588905;
 RA Kysten P., Kimbrell D.A., Daffre S., Samakovlis C., Hultmark D.;
 RT "The lysozyme locus in *Drosophila melanogaster*: different genes are expressed in midgut and salivary glands.";
 RL Mol. Gen. Genet. 232:335-343(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pranckoch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Flocker C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
 CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
 CC FOOD.
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
 CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYLGLUCURAMIC ACID IN PEPTIDOLYCAN
 CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
 CC -!- TISSUE SPECIFICITY: ANTERIOR SECTION OF THE MIDGUT.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING ALL FEEDING STAGES OF
 CC DEVELOPMENT IN BOTH LARVAE AND ADULT.
 CC -!- INDUCTION: REPRESSED WHEN BACTERIA ARE INJECTED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; X58382; CAA41272.1; -
 CC EMBL; AE003470; AAF47450.1; -
 CC PIR; S20914; S20914.
 CC HSP; P11941; 1LMC.
 CC FlyBase; FBgn0004427; LysD.
 CC InterPro; IPR001916; -
 CC Pfam; PF00062; Lys; 1.
 CC PROSITE; PS00128; LACTALBUMIN_LYSOZYME; 1.
 KW HydroLase; Glycosidase; Bacteriolytic enzyme; Signal;
 KW Multigene family.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 140 LYSOZYME D.
 FT DISULFID 24 139 BY SIMILARITY.
 FT DISULFID 45 129 BY SIMILARITY.
 FT DISULFID 80 96 BY SIMILARITY.
 FT DISULFID 92 110 BY SIMILARITY.
 FT ACT_SITE 50 50 BY SIMILARITY.
 FT ACT_SITE 68 68 BY SIMILARITY.
 FT SEQUENCE 140 AA; 15635 MW; 75C24CA6F85DF903 CRC64;
 SQ

Query Match 96.8%; Score 30; DB 1; Length 140;
 Best Local Similarity 80.0%; Pred. No. 73;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
CC FOOD.
CC
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYL-MURAMIC ACID IN PEPTIDOGLYCAN
CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
CC
CC -!- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.
CC
CC -!- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD
CC LARVAL INSTAR. IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL
CC STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
CC SECOND LARVAL INSTARS.
CC
CC -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; 222223; CA80225.1; -;
CC EMBL; 222226; CA80228.1; -;
CC EMBL; AE003470; AAF47449.1; ALT_SEQ.
CC EMBL; AE003470; -; NOT_ANNOTATED_CDS.
CC PIR; S32651; S32651.
CC PIR; S32726; S32726.
CC HSSP; P11941; ILWC.
CC FlyBase; FBgn0011201; LysA.
CC FlyBase; FBgn0004426; LysC.
CC InterPro; IPR000974; -;
CC InterPro; IPR001916; -;
CC Pfam; PF00062; Lys; 1.
CC PROSITE; PS00128; LACTALBUMIN_LYSOZYME; 1.
CC Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;
CC Multigene family.
CC SIGNAL 1 18 BY SIMILARITY.
CC CHAIN 19 140 LYSOZYME A/C.
CC FT DISULFID 24 139 BY SIMILARITY.
CC FT DISULFID 45 129 BY SIMILARITY.
CC FT DISULFID 90 96 BY SIMILARITY.
CC FT DISULFID 92 110 BY SIMILARITY.
CC FT ACT_SITE 50 50 BY SIMILARITY.
CC FT ACT_SITE 58 68 BY SIMILARITY.
CC FT CONFLICT 41 42 AR -> NK (IN REF. 1).
CC SEQUENCE 140 AA; 15635 MW; 75C24CA6F85DF903 CRC64;

CC Query Match 96.8%; Score 30; DB 1; Length 140;
CC Best Local Similarity 80.0%; Pred. No. 73;
CC Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC QY 1 WSXWS 5
CC || ||
CC Db 120 WSXWS 124

CC RESULT 2
CC LYSB_DROME
CC ID LYSB_DROME STANDARD; PRT; 140 AA.
CC AC Q08694; P37158; Q9W0J8;
CC DT 01-OCT-1994 (Rel. 30, Created)
CC DT 01-OCT-2000 (Rel. 40, Last sequence update)
CC DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE LYSOZYME B PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYL-MURAMIDASE B).
GN LYSB OR CG1179.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=94211204; PubMed=8159165;
RA Daffre S., Kysten P., Samakovlis C., Hultmark D.;
RT "The lysozyme locus in Drosophila melanogaster: an expanded gene
RT family adapted for expression in the digestive tract.";
RL Mol. Gen. Genet. 242:152-162(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
CC FOOD.
CC
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYL-MURAMIC ACID IN PEPTIDOGLYCAN
CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
CC
CC -!- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.
CC
CC -!- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD
CC LARVAL INSTAR. IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL
CC STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
CC SECOND LARVAL INSTARS.
CC
CC -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; 222223; CA80225.1; -;
CC EMBL; 222226; CA80228.1; -;
CC EMBL; AE003470; AAF47449.1; ALT_SEQ.
CC EMBL; AE003470; -; NOT_ANNOTATED_CDS.
CC PIR; S32651; S32651.
CC PIR; S32726; S32726.
CC HSSP; P11941; ILWC.
CC FlyBase; FBgn0011201; LysA.
CC FlyBase; FBgn0004426; LysC.
CC InterPro; IPR000974; -;
CC InterPro; IPR001916; -;
CC Pfam; PF00062; Lys; 1.
CC PROSITE; PS00128; LACTALBUMIN_LYSOZYME; 1.
CC Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;
CC Multigene family.
CC SIGNAL 1 18 BY SIMILARITY.
CC CHAIN 19 140 LYSOZYME A/C.
CC FT DISULFID 24 139 BY SIMILARITY.
CC FT DISULFID 45 129 BY SIMILARITY.
CC FT DISULFID 90 96 BY SIMILARITY.
CC FT DISULFID 92 110 BY SIMILARITY.
CC FT ACT_SITE 50 50 BY SIMILARITY.
CC FT ACT_SITE 58 68 BY SIMILARITY.
CC FT CONFLICT 41 42 AR -> NK (IN REF. 1).
CC SEQUENCE 140 AA; 15635 MW; 75C24CA6F85DF903 CRC64;

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2001, 17:31:52 ; Search time 15.19 Seconds
 (without alignments)
 11.276 Million cell updates/sec

Title: US-09-532-263-1

Perfect score: 31

Sequence: 1 WSXWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	140	1 LYSA_DROME	P37157 drosophila
2	30	96.8	140	1 LYSB_DROME	Q08694 drosophila
3	30	96.8	140	1 LYSD_DROME	P29614 drosophila
4	30	96.8	140	1 LYSE_DROME	P37159 drosophila
5	30	96.8	142	1 LYSX_DROME	P37161 drosophila
6	30	96.8	184	1 MPL_MPLV	R40931 myeloprolif
7	30	96.8	196	1 CRBB_BOVIN	P26444 bos taurus
8	30	96.8	196	1 CRBB_HUMAN	P53672 homo sapien
9	30	96.8	196	1 CRBB_MOUSE	Q91JVI mus musculus
10	30	96.8	218	1 ALBR_KLEOX	P10488 klebsiella
11	30	96.8	222	1 PLC2_MOUSE	P09586 mus musculus
12	30	96.8	400	1 GPCR_HUMAN	P15509 homo sapien
13	30	96.8	437	1 ERL1_YEAST	P42222 saccharomyc
14	30	96.8	437	1 PROP_MOUSE	P11680 mus musculus
15	30	96.8	494	1 ADRO_MOUSE	Q61578 mus musculus
16	30	96.8	507	1 EPOR_MOUSE	P14753 mus musculus
17	30	96.8	507	1 EPOR_RAT	Q07303 rattus norv
18	30	96.8	508	1 EPOR_HUMAN	P19235 homo sapien
19	30	96.8	584	1 COB_HUMAN	P07357 homo sapien
20	30	96.8	586	1 COS_FUGRU	P07357 fuigu rubrip
21	30	96.8	595	1 SNX9_HUMAN	Q9Y5X1 homo sapien
22	30	96.8	622	1 PRLR_HUMAN	P16471 homo sapien
23	30	96.8	625	1 TPOR_MOUSE	Q08351 mus musculus
24	30	96.8	635	1 TPOR_HUMAN	P40238 homo sapien
25	30	96.8	843	1 CO7_HUMAN	P10643 homo sapien
26	30	96.8	867	1 SSPO_BOVIN	P98167 bos taurus
27	30	96.8	934	1 COB_HUMAN	P13671 homo sapien
28	30	96.8	972	1 CTA1_BACCI	P94286 bacillus ci
29	30	96.8	997	1 AT57_HUMAN	Q9UKP4 homo sapien
30	30	96.8	1077	1 SM5A_MOUSE	Q62217 mus musculus
31	30	96.8	1522	1 BAT3_HUMAN	O60242 homo sapien
32	30	96.8	1584	1 BAT3_HUMAN	O14514 homo sapien
33	29	93.5	115	1 TRN1_RABIT	P41540 oryctolagus

RESULT 1

ID	LYSA_DROME	STANDARD;	PRT;	140 AA.
AC	P37157; Q9W0J7;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	LYSOZYME A/C PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYL-MURAMIDASE A/C).			
GN	LYSA AND (LYSC OR CG9111).			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CANTON-S;			
RX	MEDLINE=942111204; PubMed=8159165;			
RA	Daffre S., Kylisten P., Samakovlis C., Hultmark D.;			
RT	"The lysozyme locus in Drosophila melanogaster: an expanded gene family adapted for expression in the digestive tract."			
RL	Mol. Gen. Genet. 242:152-162(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriel J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,			
RA	Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,			
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,			

ALIGNMENTS

THIS PAGE BLANK (USPTO)

076510 PRELIMINARY; PRT; 238 AA.
 ID 076510
 AC 076510;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE THROMBOSPONDIN-RELATED ADHESIVE PROTEIN (FRAGMENT)
 GN TRAP-C3.
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=5807;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOREDUN;
 RA Spano F., Putignani L., Crisanti A.;
 RT "Identification of a Cryptosporidium parvum putative adhesive
 RT molecule.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF073838; AAC26812.1; -;
 DR InterPro: IPR000884; -;
 DR InterPro: IPR002086; -;
 DR Pfam: PF00090; tsp.1; 2.
 DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR SMART: SM00209; TSP1; 1.
 FT NON_TER 1
 FT 238
 SQ SEQUENCE 238 AA; 26307 MW; 28242DB88F62C5A2 CRC64;

Query Match 96.8%; Score 30; DB 5; Length 238;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 DB 47 WSSWS 51

RESULT 15

Q19092 PRELIMINARY; PRT; 254 AA.
 ID Q19092
 AC Q19092;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE SIMILAR TO THROMBOSPONDIN.
 GN F01F1.13.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP *SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Miller N.;

RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U13070; AAC46484.1; -;
 DR InterPro: IPR000884; -;
 DR Pfam: PF00090; tsp.1; 2.
 DR SMART: SM00209; TSP1; 1.
 SQ SEQUENCE 254 AA; 29602 MW; F2DD714CDA62D9D6 CRC64;

Query Match 96.8%; Score 30; DB 5; Length 254;
 Best Local Similarity 80.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 DB 58 WSTWS 62

Search completed: August 24, 2001, 17:34:11
 Job time: 154 sec

```

RA Fuh G., Wells J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
   cancer cell lines.";
RL J. Biol. Chem. 270:13133-13137(1995).
DR EMBL: S78505; AAB34470.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003528; -.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
FT NON_TER 1
SQ SEQUENCE 206 AA; 23950 MW; CED939781B3C804E CRC64;

Query Match          96.8%; Score 30; DB 4; Length 206;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 191 WSAWS 195

RESULT 11
Q27950
ID Q27950 PRELIMINARY; PRT; 229 AA.
AC Q27950;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EPOR.
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B., F Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61398; AAB03870.1; -.
DR HSSP: P19235; 1EBA.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003528; -.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
FT NON_TER 1
SQ SEQUENCE 229 AA; 25196 MW; F6E01C4AB07893E8 CRC64;

Query Match          96.8%; Score 30; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 175 WSAWS 179

RESULT 12
Q28206
ID Q28206 PRELIMINARY; PRT; 229 AA.
AC Q28206;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

```

```

DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EPOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B., F Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61399; AAB03871.1; -.
DR HSSP: P19235; 1EBA.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003528; -.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
FT NON_TER 1
SQ SEQUENCE 229 AA; 25170 MW; EDFAA6F110D992E2 CRC64;

Query Match          96.8%; Score 30; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 175 WSAWS 179

RESULT 13
Q97888
ID Q97888 PRELIMINARY; PRT; 234 AA.
AC Q97888;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE INTERLEUKIN-4 RECEPTOR ALPHA CHAIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC Trigona W.T., Estes D.M.;
RT "Cloning of bovine homolog to interleukin-4 receptor alpha chain.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081273; AAD16011.1; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26722 MW; B068385D2C86EE1B CRC64;

Query Match          96.8%; Score 30; DB 6; Length 234;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 183 WSAWS 187

RESULT 14

```

```

RX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20389602; PubMed=10930736;
RA Pedraza-Diaz S., Amar C., McLauchlin J.;
RT "The identification and characterisation of an unusual genotype of
RT Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
RL FEMS Microbiol. Lett. 189:189-194(2000).
DR EMBL; AF248744; AAG01093.1; -.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 18614 MW; F2AD32849A8B5E9C CRC64;

Query Match          96.8%; Score 30; DB 5; Length 168;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 143 WSSWS 147

RESULT 7
Q9GZ22 ID Q9GZ22 PRELIMINARY; PRT; 168 AA.
AC Q9GZ22;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE THROMBOSPONDIN-RELATED ADHESIVE PROTEIN (FRAGMENT).
GN TRAP-C1.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20389602; PubMed=10930736;
RA Pedraza-Diaz S., Amar C., McLauchlin J.;
RT "The identification and characterisation of an unusual genotype of
RT Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
RL FEMS Microbiol. Lett. 189:189-194(2000).
DR EMBL; AF248745; AAG01094.1; -.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 18698 MW; 2D02BC437C2AA44D CRC64;

Query Match          96.8%; Score 30; DB 5; Length 168;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 143 WSSWS 147

RESULT 8
Q9GZ21 ID Q9GZ21 PRELIMINARY; PRT; 168 AA.
AC Q9GZ21;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE THROMBOSPONDIN-RELATED ADHESIVE PROTEIN (FRAGMENT).
GN TRAP-C1.
OS Cryptosporidium meleagridis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=93969;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20389602; PubMed=10930736;
RA Pedraza-Diaz S., Amar C., McLauchlin J.;
RT "The identification and characterisation of an unusual genotype of
RT Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
RL FEMS Microbiol. Lett. 189:189-194(2000).
DR EMBL; AF248746; AAG01095.1; -.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 18576 MW; CE9516EE86479C3 CRC64;

Query Match          96.8%; Score 30; DB 5; Length 168;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 143 WSSWS 147

RESULT 9
Q65971 ID Q65971 PRELIMINARY; PRT; 191 AA.
AC Q65971;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 21.2 KDA PROTEIN.
OS cucurbit aphid-borne yellows virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Luteovirus.
OX NCBI_TaxID=91753;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N;
RX MEDLINE=94303150; PubMed=8030201;
RA Guillely H., Wipf-Scheibel C., Richards K., Lecoq H., Jonard G.;
RT "Nucleotide sequence of cucurbit aphid-borne yellows luteovirus.";
RL Virology 202:1012-1017(1994).
DR EMBL; X76931; CAA54253.1; -.
DR InterPro; IPR000515; -.
DR InterPro; IPR001964; -.
DR Pfam; PF01659; Luteo_Vpg; 1.
DR PRINTS; PR00912; LVIRUSORF5.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 191 AA; 21154 MW; E0C64CC99E555520 CRC64;

Query Match          96.8%; Score 30; DB 14; Length 191;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 97 WSSWS 101

RESULT 10
Q16354 ID Q16354 PRELIMINARY; PRT; 206 AA.
AC Q16354;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95286597; PubMed=7768908;
```

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TRAP-C1 (FRAGMENT).
GN
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P12 (NATURAL ISOLATE);
RA Spano F., Putignani L., Guida S., Crisanti A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF033829; AAB92610.1; -
DR InterPro; IPR000884; -
DR SMART; SM00209; TSP1; 1.
FT NON_TER 1
FT NON_TER 72
FT NON_TER 72
SQ SEQUENCE 72 AA; 7564 MW; 7D2AED67148F1518 CRC64;

Query Match 96.8%; Score 30; DB 5; Length 72;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
|| ||
Db 16 WSTWS 20

RESULT 3
Q9H2J5 PRELIMINARY; PRT; 97 AA.
AC Q9H2J5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MITOGALIGIN.
GN GALIG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Legrand A., Guittaut M., Charpentier S., Normand T., Dubois M.,
RA Rainond J.;
RT Identification of an internal gene to the human Galectin-3 gene
RT encoding two novel proteins from different overlapping reading
RT frames.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF266280; AAG44702.1; -
SQ SEQUENCE 97 AA; 11168 MW; B9CF5CECAEA7C055 CRC64;

Query Match 96.8%; Score 30; DB 4; Length 97;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
|| ||
Db 44 WSTWS 48

RESULT 4
Q61427 PRELIMINARY; PRT; 147 AA.
AC Q61427;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PROCOLLAGEN, TYPE I, ALPHA 1 (ALPHA 1 TYPE I COLLAGEN) (FRAGMENT).
GN COL1A1 OR COL1A1.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE=LIVER;
RX MEDLINE=94344105; PubMed=8065328;
RA Rhodes K., Rippe R.A., Umezawa A., Nehls M., Brenner D.A., Breindl M.;
RT "DNA methylation represses the murine alpha 1(I) collagen promoter by
RT an indirect mechanism";
RL Mol. Cell. Biol. 14:5950-5960(1994).
DR EMBL; X54876; CAA38657.1; -
DR MGD; MGI:88467; Col1a1.
DR InterPro; IPR001007; -
DR Pfam; PF00093; vwc; 1.
DR PROSITE; PS01208; VWFC; 1.
DR SMART; SM00214; VWC; 1.
FT NON_TER 147
FT NON_TER 147
SQ SEQUENCE 147 AA; 16652 MW; 9263BF0A91B4307D CRC64;

Query Match 96.8%; Score 30; DB 11; Length 147;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
|| ||
Db 132 WSSWS 136

RESULT 5
Q38069 PRELIMINARY; PRT; 162 AA.
AC Q38069;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE TAIL TUBE PROTEIN (GPFI).
GN FII.
OS Bacteriophage PSI7.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
OX NCBI_TaxID=33710;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Shinomiya T., Kumazaki T., Mohri N., Ishii S., Arisaka F.;
RT "Nucleotide sequence of the contractile tail sheath and tube genes of
RT bacteriophage PSI7 and the amino acid sequence of the gene products.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; D26449; BAA05468.1; -
SQ SEQUENCE 162 AA; 17688 MW; 8275079A1C2E8FE6 CRC64;

Query Match 96.8%; Score 30; DB 9; Length 162;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
|| ||
Db 55 WSWS 59

RESULT 6
Q9GZ23 PRELIMINARY; PRT; 168 AA.
ID Q9GZ23
AC Q9GZ23;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE THROMBOSPONDIN-RELATED ADHESIVE PROTEIN (FRAGMENT).
GN TRAP-C1.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2001, 17:31:37 ; Search time 37.87 Seconds
(without alignments)
17.468 Million cell updates/sec

Title: US-09-532-263-1
Perfect score: 31
Sequence: 1 WSXWS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	52	4	Q16340
2	30	96.8	72	5	Q43983
3	30	96.8	97	4	Q942J5
4	30	96.8	147	11	Q61427
5	30	96.8	162	9	Q38069
6	30	96.8	168	5	Q9GZ23
7	30	96.8	168	5	Q9GZ22
8	30	96.8	168	5	Q9GZ21
9	30	96.8	191	14	Q65971
10	30	96.8	206	4	Q16354
11	30	96.8	229	6	Q27950
12	30	96.8	229	6	Q28206
13	30	96.8	234	6	Q97888
14	30	96.8	238	5	Q76510
15	30	96.8	254	5	Q19092
16	30	96.8	291	5	Q20991
17	30	96.8	294	2	Q9RMF3
18	30	96.8	304	5	Q9XU51
19	30	96.8	316	11	Q35545

20	30	96.8	328	4	O95061
21	30	96.8	332	14	Q82493
22	30	96.8	349	4	Q9UHQ5
23	30	96.8	367	1	O59408
24	30	96.8	375	9	Q9ZX59
25	30	96.8	388	1	Q9VIG1
26	30	96.8	394	2	O33205
27	30	96.8	422	4	Q16542
28	30	96.8	425	6	O02661
29	30	96.8	428	5	Q9VN52
30	30	96.8	432	11	P70225
31	30	96.8	432	11	O64385
32	30	96.8	437	3	Q12007
33	30	96.8	446	4	O43384
34	30	96.8	455	3	O08231
35	30	96.8	509	6	Q9MY29
36	30	96.8	528	2	P70733
37	30	96.8	558	5	Q9V7B4
38	30	96.8	558	13	Q9PVW6
39	30	96.8	579	10	Q9STS3
40	30	96.8	588	13	Q9PVW7
41	30	96.8	612	8	Q9MQV2
42	30	96.8	622	6	Q9N0J7
43	30	96.8	633	4	Q9Y590
44	30	96.8	647	5	Q9U217
45	30	96.8	654	5	Q19284

ALIGNMENTS

RESULT 1

Q16340 ID Q16340 PRELIMINARY; PRT; 52 AA.
AC Q16340;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PHOSPHODIESTERASE BETA-SUBUNIT PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95322980; PubMed=7599633;
RA Bayes M., Giordano M., Balcells S., Grinberg D., Villageliu L.,
RA Martinez I., Ayuso C., Benitez J., Ramos-Arroyo M.A., Chivelet P.,
RA Et AL.;
RT "Homozygous tandem duplication within the gene encoding the beta-
RT subunit of rod phosphodiesterase as a cause for autosomal recessive
RT retinitis pigmentosa";
RL Hum. Mutat. 5:228-234(1995).
DR EMBL; S78008; AADI4270.1; -.
FT NON_TER 1
SQ SEQUENCE 52 AA; 6124 MW; 4FC1A6A8C9DAEF94 CRC64;

Query Match 96.8%; Score 30; DB 4; Length 52;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 42 WSXWS 46

RESULT 2

O43983 ID O43983 PRELIMINARY; PRT; 72 AA.
AC O43983;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)